

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGGCGGAGCAGCACGGCCGCAGGACCTGGAGCTCCGGCTGCGTCTTCCG
CAGCGCTACCCGCCATGCGCCTGCCGCCGGCGCTGGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAAGCCGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAAGAAACTTGGCGGGGGAAACA
CGGCTTGGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCGAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATCGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGAGCAGACA
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCTGTGGATGTGGACGAGTGTGCGGCCGAGCCGCCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACGAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGCTGACGGCTTCGAAGAAACG
GAAGATGCCGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCCACACAGCT
GCCCTCCCGCAAGACCTGTAATGTGCCGGACTTACCCTTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAAC
TTGGCCGCCATGGCCAACTTGTTTATTGCAGCTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTGATTCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCGGATCGGAATTAAATTGCCGCAGCACCATGCCGTGAAAT
AACCTCTGAAAGAGGAACTTGGTTAGGTACCTCTGAGGCGGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGAAAGTCCCCAGGCTCCCCAGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLLPAPPEAAKKPTPCHRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSKYESSEIRL
LEILEGLCESSDFECNQMLEAQEEHLEAWWLQLKSEYPDLFEWFCVKTLVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSGDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCGTLNRDCGECEVGWLDE
GACVDVDECAAEP PCSAAQFCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TGCACCTCGTTCTATCGATTGAATTCCCCGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACGCGTCCGCCAGGCCGGAGGCAGCGGCCAGCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGACTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCTGAGCAGCAGATGGCCGGAGGAGCGCCTTC
CCTGCCGCCCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCAGGCCGGAGGC
CGGGCCGCCAGGAGGAGACCTGTACCTATGGATCGATGCTCACCAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTAGAGGGAAAATGGCACCTTTACACATGAT
TTCAGAAAAGCGAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTCAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGCTTGTGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCCTCTGCTGGAAACAGTGCCTCACAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTGCCCAGGCAGGTGCCAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCGAGTGTCCCTGATGGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAAC TGTGACAAAGCAAACCTGCTCAACCACCTGCTTTAATGGAGGGACC
TGTTCTACCCCTGGAAAATGTATTGCCCTCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCCTGTCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCGAGGAGACCTCTGTTCAAAGCCTGTGCGAGCCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAACAAATGCCAATGTCAAGAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACTGCCCTGAGGCCAGCAGGCGCCAGCTCAGGCAGC
ACACGCCCTCACTTAAAGGCCAGGGAGCGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTGTAAACCTTCA
TGTGTTGAATGTTCAAATAATGTTCATTACACTTAAGAATACTGGCCTGAATTTTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTCCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTGTGTTAGTGGCAGATATTCAAACATTACAATGCATTATGGT
TCAGGTTAAATTTCACTGAGCTGTTAGTGGCAGATATTCAAACATTACAATGCATTATGGT
GTCTGGGGCAGGGAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCAAGATTATTGTCAAGATATTAGAT
GTTTGTACATTAAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACC
TTACCAATTCCAGAGATTCACTGTTAAACAAAAAAATTACACTGTGGTAGTGGCATT
AAACAAATATAATATTCTAAACACAATGAAATAGGGAAATATAATGTATGAACCTTTGCA
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAACATTTAT
ACTGTTGTATGTATAAAATAAGGTGCTGCTTAGTTTTGAAAAA
AAAAAAAAAAAAAAAAAGGCCGGCGCAGCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCAAC TTGTTATTGCAGCTTATAATG

FIGURE 4

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPPLL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKCI GKS KCKCSKG YQGDLC SKPVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW
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Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGGTGGCGTCCGGCGTCAGAGCCAGGAGGCCAGGGCGCGGGCCAGCCTGGG
CCCCAGCCCACACCTCACCAAGGGCCAGGAGCCACC**ATGT**GGCGATGTCCACTGGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGCTGTGGCGCCGG
GAGCTAGCACCAGGGTCTGCACCTGCAGGGCATCCGGACGCCAGGGAGGCCGGTACTGCCAGGA
GCAGGGACCTGTGCTGCCGCGGCCGTGCCGACGACTGTGCCCTGCCACTCGGGGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGCTCCGACTGCTGCCCTGACTTCTGGGACTTC
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTGGAAACGTACTGGACAACACTGTAACC GTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGCATGACCCTGG**ATGAGGGCATTG**CTACCGCCTGGGCACCA
TCCGCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGCTGAACCCAGGGAG
GTGCTCCACAGCCTCGAGGCCTCTGAGAAAGTGGCCAACCTGATTGATGAGCCTTGA
CCAAGGCAACTGTGCAGGCTCTGGGCCTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTGCTGTGCCAGAACCTGCTGTCTGTGAC
ACCCACCAGCAGCAGGGCTGCCGCGTGGCGTCTCGATGGTGCCTGGTGGTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACAATGACATCTACAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATAACGCCGATGGGACCCACTCAGTCAAGATCACAGGATGGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTCAAATACTGGACTGCCCAACTCCTGGGCC
CAGCCTGGGCGAGAGGGCCACTTCCGCATCGTGCAGGCCGTCAATGAGTGCACATCGAG
AGCTCGTGTGGCGTCTGGGCCGCGTGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACGCCGGCTGGGATCCAGGCTAAGGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGCCGGCGCAGGCCGGCGCCAGGGCGCTAAT
CCCGCGCGGGTCCGCTGACGCAGGCCCGCTGGAGGCCGCGAGGCGAGACTGGCG
GAGCCCCAGACCTCCCAGTGGGACGGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCCTGGGCCCCCCACTCAAGACTACCAAAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATAACCCACCCAAATCCGTATTCTTTTTTTTTAGACAGGGTCTTGCTCCG
TTGCCAGGGTGGAGTGCAGTGGCCCATCAGGCTCACTGTAACCTCCGACTCCTGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGACTACAGGTGCACCCACACCTGGC
TAATTTGTATTTGTAAAGAGGGGGTCTCACTGTGTTGCCAGGCTGGTTCGAACT
CCTGGGCTCAAGCGGTCCACCTGCCTCCGCTCCAAAGTGTGGATTGCAGGCATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTTCACTGTTAAAAA
TAAAACCAAAAGTATTGATAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18359, pI: 7.45, NX(S/T): 1
MWRCPLGLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYEQDLCCRGRADDC
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGYWDNCNR
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCCTGGTGGTCTCGCTGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACGCCCTGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTGGG
AGGCCAGAGAGATAACGCCGGCATGGACCCACTCAG

FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGACTGCCTGCAGGTGGAGAACTGCACCCAGCTGGGG
GAGCAGTGCTGGACCGCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGATGACTCACAGGACTACTACGTGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGGGGCCATGCCTGCAGCCGGCTGCCGCCATCCTT
GCGCTGCTCCCTGCACTCGGCCTGCTGCTCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGTGGGAGCCTGTCCTGGTTCCCTGAGGCACATCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCTGACCCCTCCATGGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCCAACCCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCCTAACCCCTGTGCTCAGGCACCTCTTCCCCCAGGAAGCCTT
CCCTGCCACCCCATCTATGACTTGAGCCAGGTCTGGTCCGTGGTGTCCCCCGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCCAGTAAGGCTGAGATGAAGTGGACTGAGTAGAACTGGA
GGACAAGAGTCGACGTGAGTTCTGGAGTCTCCAGAGATGGGCCTGGAGGCCTGGAGGAA
GGGCCAGGCCTCACATTGTTGGCTCCCTGAATGGCAGCCTGAGCACAGCGTAGGCCCTT
AATAAACACCTGTTGGATAAGCCAAAAAA

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSGDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFHGPAGSTLNPLVRLHLPQEAFPAHPIYDLSQVWSVSPAPSRGQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

FIGURE 10

CCACCGCGTCCGAAACCTCTCCAGCGAGGGAGCCGCCGCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCCGAGTACCAACTCTACAGCAGGACCAGTGGCAAGCA
CGTCAGGTCAACGGCGTGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGTTCGCATCAAAGGGCTGAGAGTGAGAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTGTTCACGGAGATCGTGGAGAACAACTATACGGCCTTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACCGGCAGGGCGGCCAGGCTTCCGCAGCCGCCAGAAC
CAGCGCAGGCCACTTCATCAAGCGCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAAGCAGAAGCAGTCGAGTTGTGGCTCCGCCACCCGCCGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGCCCTGGCCGCTCCC
CACCCCTTCCCTCTTAATCCAAGGACTGGCTGGGTGGCGGGAGGGAGCCAGATCCCC
GAGGGAGGACCTGAGGGCCCGAAGCATCCGAGCCCCAGCTGGAAAGGGCAGGCCGGT
CCCCAGGGCGGCTGGCACAGTGCCCTTCCGGACGGTGGCAGGCCCTGGAGAGGA
GAGTGTCAACCTGATCTCAGGCCACCAGCCTCTGCCGGCTCCAGCCGGCTCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCC
TCTGCTTCTCGGATCTCCCTCAGTCTGCCAGCCCCAAACTCCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTCAAGAAAAAGAAAGGGAGAGAGAGGAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCAACTCCCAGCCC
CGGAATAAAACCATTTCCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDCVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAAATTCTCCCTGTTGAATTTCGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTCTGGACTTCAACAGAACCCCATCCAGT
CATTTGATTGCTGTTATTTTTCTTTCTTTCCCACCACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTCCCT
GAAGTCTTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGCAAACCTCTGGCCTGCC
CTAGTGTGTGCCGCTGCGACAGGAACCTTGTCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCCAGGGCGTAACCGTACTCTACCTCCACAACAACCAAATTAAATAATGC
TGGATTTCCTGCAGAACTGCACAATGTACAGTCGGTGCACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTCCCAAAGAATGTCAGAGTCTCCATTGCAGGAAAC
AATATTCAAGACCATTTCACGGCTGCTTGCCCCAGCTTGAAGCTGAAGAGCTGCACCT
GGATGACAACCTCATATCCACAGTGGGGTGGAAAGACGGGCCTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCCTGGCTTGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTATATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTATTGTTGGACGGAACCTCTGACCAACAAGGGTATGCCG
AGGGCACCTTCAGCCATCTCACCAAGCTCAAGGAATTTCATTGTACGTAATTGCTGTCC
CACCCCTCCTCCGATCTCCAGGTACCGATCTGATCAGGCTCTATTGCAAGGACAACAGAT
AAACCACATTCCCTTGACAGCCTCTCAAATCTCGTAAGCTGGAACGGCTGGATATATCA
ACAACCAACTCGGGATGCTGACTCAAGGGTTTTGATAATCTCTCAAACCTGAAGCAGCTC
ACTGCTCGGAATAACCTTGGTTTGACTGCACTTAAATGGGTACAGAATGGCTCAA
ATATATCCCTCATCTCAACGTGCCGGGTTCATGTGCCAAGGTCTGAACAAAGTCCGG
GGATGGCCGTAGGGAAATTAAATGAATCTTGTCCCTGTCCACCACGACCCCCGGCCTG
CCTCTCTTACCCCAAGCTACAGCTCTCCGACCAACTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAAAGCTACACGCCCTCAAACCTTACACATCGAAACTCCACGATTC
CTGACTGGGATGGCAGAGAAAGAGTGAACCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTGAATGATACTTCCATTCAAGTCAGCTGGCTCTCTCTTACCGTGATGGCATA
CAAACTCACATGGGTGAAATGGCCACAGTTAGTAGGGGCTCGTCAAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACTTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGCTTTAACTACCGCGCGGTAGAAGACACCATTGTCAGAGGC
CACCAACCATGCCCTCATCTGAACACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGCGGGCTGATCGGGGGCGGGTATATT
GTGCTGGTGGCTTGCTCAGCGTCTTGTGCTGGCATATGCACAAAAGGGGCGCTACACCTC
CCAGAAGTGGAAATAACACGGGCGGGCGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCATCTGGAGATGACAGAAACCAAGTTTCAGATCGTCTCTTAAATAACGAT
CAAACCTTAAAGGAGATTCAAGACTGCAGCCATTACACCCAAATGGGGCATTAAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACACAGCAGCGTGCCAGACCTGGAGC
ACTGCCATACGTGACAGCCAGAGGCCAGCGTTATCAAGGCGGACAATTAGACTCTTGAGAA
CACACTCGTGTGCACTAAAGACACGCAGATTACATTGATAAAATGTTACACAGATGCAT
TTGTCATTGAATACTCTGTAATTATAACGGTGTACTATATAATGGGATTAAAAAAAGTG
CTATCTTCTATTCAAGTTAATTACAAACAGTTGTAACCTTGTCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGaffFLKSwLIISLGLySQVSKLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTvLYLHNNQINNAGFPaelHNvQSVHTVYLYGNQLDEFPMNLPKNvRLHLQENNIQTI
SRAALAQLLKEELHLDdnsISTVGVEDGAFREAIslKLLFLSKNHLSVPVGLPVDLQELR
VDENRIAVI SDMAFQNLTSLERLIVDGNLLTNKGIAEGTFShLTKLKEFSIVRNLSLHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARN
PWFCDCS1KvWTEWLKYIPSSLNVRGFMCGPEQVRGMARvELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTTskLPTIPDWDGRERVTppIseriqlsIHvND
TSIQVSWLsLFTvMAYKLTWvKMGHSLVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNYRAvEDTICSEATTHASyLNNGNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVvVL
LSVFCWHMhKKGRYTSQKwKYNRGRRKDDYCEAGTKKDnsILEMTEtsFQIVSLNNdQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCCGCCTCCACGAGCG
ATCCCCGAGGGAGGCCGCGGCCCTCGCGAGGCAGAGGGCCGACGAGGAAGACCCGGGTGGCTGCGCCCTGCC
TCGCTTCCCAGCGCCGGCTGCAGCCTGCCCCTCTGCTGCCCTGAAAATGGAAAAGATGCTCGCAGGCT
GCTTCTGCTGATCCTCGGACAGATCGTCTCCTCCCTGCCAGGGCAGGGAGCGGTACAGTGGGAGGTCCATCT
CTAGGGGAGACACGGCTGGACCCACCCGAGCGGCCCTCTGGAGAGTCTCTGTGAGAACAAGCGGGCAGACC
TGGTTTCATCATTGACAGCTCTCGCAGTGTCAACACCCATGACTATGCAAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCATTCTGGACATTGGTCTGTGTCACCCGAGTGGGCTGCTCCAATATGGCAGCACTGTCAAGGAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCTGTCAAGAGGATGCGGCATCTGTCCACGG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAAAGCAGAGGGGGCCGGCCCTG
GGGAGAATGTGCCACGGGTACATAATGATCGTACAGATGGAGACCTCAGGACTCCGTGGCGAGGGTGGCTGCTA
AGGCACGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCCTCCTGTGGCAATTCAAGCCAGATTGAGACGCTGACCTCCGTGTC
AGAAGAAGTTGTGACGGCCACATGTGCAGCACCTGGAGCATAACTGTGCCACTCTGCATCAACATCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCGAGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTGCTCAGTGTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGACTACTGTGCCCTAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCATGAAGGATTGCTCTTAACCCAGATGAAAAAA
CGTGCACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTCAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCCAATGGAAAACCTGCAGCCAGTGGACCACTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACCGGAGGATTCTCGTGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGCTCCGGGTGGATTACTGCCCTGCTGAGTGACCATGGTTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCTGCTGAGTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
CAAATGGACTCTTGTGCTGGGGGACACGGTTGTGAACATTGTGTGAAGCAGTGAAGATTGTTGTG
GCCAGTGTGAAAGGTTATATACTCCGTGAACAGTGAACACTCATACACGTGCGAGTGTGCTGGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCAATCAACCCACCATGGCTGCCAACACATTGTGTTA
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGATTGTTCTAGCTGAGGACGGAAAGACGGTGCAGAAT
GCACGTGAAAGGCCAATTGACCTGGCTTTGTGATCGATGGATCCAAGAGTCTGGAGAAAGAGAATTGGAGGTG
TGAAGCAGTTGTCACTGAAATTAGATTCTGACAATTCCCCAAAGCCGCTCGAGTGCTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTTCACTCTGAGAAACCTCAACTCAGCCAAGACATGAAAAAGCCGTGGG
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGACCAGCCATTGTTCAACGGACGGCTCAGGATG
ACGTCCTCGAGTGGGCCAGTAAAGCCAAGGCCAATGGTATCACTATGTATGCTGTTGGGGTAGGAAAAGCCATTG
AGGAGGAACATACAAGAGATTGCCCTGAGCCCACAAACAAGCATCTTCTATGCCGAAGACTTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGGAACTGCCAAAAACGGTCCAACAGCCAACAGAATCTGAGCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAATTGCACTGAGATAACAGATATTGTTGAAGAAGACAATTGTTACGGCTACACAAAGCTTT
CCCATTCAACAAACCTTCAGGAAGGCCCTTGAAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCACAGAACAGAAGTAAAGAAAATTAAACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGGCC
TGGAAAATGCCCTGAGATAACAGATGAAGATTAGAAATCGGACACATTGAGTCATTGTATCACGGATTACAAT
GAACGCAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGTGAAGTAAACAAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTATACTACTAACTGTATAAATTATCTAGGAAAAAAACCT
TCAGAATTCTAAGATGAAATTACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC
AACTGCTCTGCCTCATCCTGCCTAGTGTGCAATCTCATTGACTATACGATAAAAGTTGCACAGTCTTACTT
CTGAGAACACTGCCATAGGAAATGCTGTTTTGTACTGGACTTACCTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGTGGAACAAGTGGATTTTATACAATATTAACATTAAACACTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSGRSISRGRHARTHPOQTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFSLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGLRLENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIQVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKLCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIQDLCAMEDHNCEQLCVNVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKGPGC
EHECVNMEESYYCRCHRGYTLDPNGKTCRSVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSRGKTCAKLDSCALGDHGCE
HSCVSSEDFVCQCFCFGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRLA
EDGKRCRRKDVKSTHHGCEHICVNNNGNSYICKCSEGFVLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVVKQFVTGIIDSLETISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEELQEIASEPTNKHLYAEDFSTMDEISEKLKKGICEALEDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGCTCGGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGGC
CATGATTCCTCCCTCCGGGCCCCCTGGTACCAAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGCGGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTCTTCCAGCGTGGTACACCTGCACGGGAGGGTGTCTTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTCTTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCCTGCCAGCTCCATCCTGCCGTCTCAGGGTGTGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGGCAAATCTAGGGCCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCATCCTGCCGTCTCAGGGTGTGCCCTA
GTGGGGCAAACGTGACCCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGCTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCAAGCATTAGATGTCATCCGTG
GGTCTTAAGCCTCACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGCCCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGGTACCCCTGGTGGACTGGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCAACGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCCTGCCCTGCCCAAGAGCTCAGACACAATCTCAAGAATGGGACCC
TTCCTCTGTCACCTCCGCACGAGCCCTCCGCCACCCATGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCCTCACTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT
ATTGATATAACCTGTCAAGCTGGCTGGTTAGGTTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTTTCAATTGCAAATTAAATAAGATAACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGLQEKDGGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSLTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTILVGLGLLAGLVLLYHRRGKALEEPANDIKEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262,
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTCGGGCACCGCCA**ATGAAACGCCTCCGCTCTAGGGTTTTCCACTTTG**
TTGAATTGTCCTATACTCAAAATTGCAACAGACACCTGTCTCCAAATGAAAATGTGA
AATACGCAATGGAATTGAAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGAAATTAACTCAGTCCTGTGGAAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTGTATGTGTACCTGGCTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGCCATT
TAGATAATGTCTGTATAGCTGCAAATTAAATAAAAACCTTAACAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTAGAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTTCATTACTAGGTTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCCTTCTAACTCAACTCTACTGAATTGTAACCAACCGTGAAT
AATTTGTTCAAAGGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCACTCCTCATATGAATATGGATGGAGACTACATAAATATA
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGAGTTGCATTTCATTTATATA
AGAGTATTGGCCTTGCTTCATCATCTGACAACCTTCTTATTGAAACCTCAAAATTATGAT
AATTCTGAAGAGGGAGGAAAGAGTCATATCTTCAGTAATTTCAGTCTCAATGAGCTCAAACCC
ACCCACATTATATGAACCTGAAAAAAATAACATTACATTAAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCTTTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCT
GACACATTGCAATTGATGTCCTCTGGCCTTCATTGGTATTAAAGATTATAATATTC
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGCTTGCCATATGCATTTT
ACCTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCAACAAAATCTTGCTG
TAGCCTATTCTTGCTGAATTGTTCTTGGATCAATACAAATACTAATAAGCTCT
TCTGTTCAATCATTGCCGACTGCTACACTACTCTTTAGCTGCTTTGCATGGATGTGC
ATTGAAGGCATACATCTCATGTTGTTGGGTGTCATCTACAACAAAGGGATTTGCA
CAAGAATTTTATATCTTGCTATCTAACGCCAGCCGGTAGTTGGATTTGGCAGCAC
TAGGATACAGATATTATGGCACAACCAAAGTATGTTGGCTTAGCACCGAAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCTAATCATTCTGTTAATCTCTGGCTTTGGAGTCAT
CATATACAAAGTTTCGTACACTGCAGGGTTGAAACCAGAAGTTAGTTGCTTGAGAAC
TAAGGTCTTGCAAGAGGGAGCCCTCGCTCTCTGTTCTCGGCACCACCTGGATCTT
GGGGTTCTCCATGTTGTCACGCATCAGGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGATGTTCATTTTTATTCTGTGTTGGATGTTAAGG**TAAACATAGAGAAT**
ATTACAGATTGTTCAAAATGCCCCGTTGTTGGATGTTAAGG**TAAACATAGAGAAT**
GTGGATAATTACAACGTGACAAAAATAAAATTCCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCAATTAAACTACTAGACAAAAAGTATTAAATCAGTTTCT
GTTATGCTATAGGAACGTAGATAATAAGGAAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTCTGTCAAAATAGTATTGCAAGATATTGAAAGTAATTGGTT
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACCTCGGTAAATGAGCTCCATTACAGAAAGTGGAACATAAGAGAATGAAGGGCAGA
ATATCAAACAGTAAAAGGAATGATAAGATGTATTGAAATGAACTGTTCTGTAGAC
TAGCTGAGAATTGTTGACATAAAAGAATTGAAGAACACATTTCACCATTGAA
TTGTTCTGAACCTAAATGTCCACTAAAACAACCTAGACTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAGGTTACCTCCACAAATTGAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLLVFSTLLNCSYTQNCTKTPCLPNAKCEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFVKTVNNFVQRDTFVVWDKLSVNHRRTLTKLMHTVEQATLRIQSFKTTEFDT
NSTDIALKVFVFFDSYNMKHIHPHMNMDGYINIFPKRKAAYDSGNVAVAFLYYKSIGPLLS
SSDNFLLKPQNYDNSEEERVISSVISVSMSSNPPTLYELEKITFTLSHRKVTDRYRSLCAF
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPAVVVGFSAA LGYRYYGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATTTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGCAATGTTGCAGTGCATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCCATCATCTGACAACCTCTATTGAAACCTAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCACTGAGCTCAAACCCACCCAC
ATTATATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTGGAAACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTTCCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACGTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTTCAGTGAATTCAAAGCACCAGGA

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FIGURE 21

GCTCCCAGCCAAGAACCTCGGGGCCGCTGCGCGTGGGGAGGAGTTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCTCCGCAGATCCGAACGGCTGGGCGGGTCAACCCGGCTGGGA
CAAGAAGCCGCCGCTGCCTGCCCGGGCCGGAGGGGGCTGGGCTGGGCGGGAGGCAG
GGTGTGAGTGGGTGTGCGGGGGCGGAGGCTTGATGCAATCCGATAAGAAATGCTCGGG
TGTCTGGCACCTACCGTGGGCCGTAAGCGCTACTATATAAGGCTGCCGCCGGAG
CCGCCGCCGTCAGAGCAGGAGCGCTGCCTCAGGATCTAGGGCCACGACCATCCAAACCC
GGCACTCACAGCCCCGAGCGCATCCGGTCCGCCAGCCTCCGCACCCCCATGCCGG
AGCTGCGCCGAGAGCCCCAGGGAGGTGCCATGCGGAGCGGGTGTGGTGGTCCACGTATGG
ATCCTGGCCGGCCTCTGGCTGGCGTGGCCGGCGCCCCCTCGCTTCTCGGACGCCGGGCC
CCACGTGCACTACGGCTGGGGCGACCCCATCCGCCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTCTCCAGCTGCTTCTGCCGATCCGTGCCGACGGCGTCGTGGACTGCCGCCGG
CAGAGCGCGCACAGTTGCTGGAGATCAAGGCAGTCGCTCTGCCGACCGTGGCATCAAGGG
CGTGCACAGCGTGCCTGACCTCTGCATGGCGCCGACGGCAAGATGCAGGGCTGCTTCAGT
ACTCGGAGGAAGACTGTGCTTCGAGGGAGGAGATCCGCCAGATGGCTACAATGTGTACCGA
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTCCAAACAGCGGCAGCTGTACAAGAA
CAGAGGCTTCTTCACTCTCATTTCTGCCCATGCTGCCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTTCGCCCTGGAGACCGACAGCATG
GACCCATTGGGCTTGTACCCGGACTGGAGGCCGTGAGGAGTCCAGCTTGGAGAAGTAAC
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTTACCTGCAGCGTGGGGACG
TGCTTCTACAAGAACAGTCCGTAGTCCACGTTCTGTTAGCTTAGGAAGAACATCTAGAA
GTTGTACATATTCAAGAGTTCCATTGGCAGTGCCTAGTTCTAGCCAATAGACTGTCTGAT
CATAACATTGTAAGCCTGTAGCTTGCCTGCCAGCTGCTGCCCTGGGCCATTCTGCTCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCTGAGTTCTGTTGAATACCTCCATCGATGGGAAC
TCACTTCTTGGAAAAATTCTTATGTCAAGCTGAAATTCTCTAATTTCAGGAACAGGTGATCCACTCTGTA
CCCAGGAGCAGCCAGAAGACAGGCAGTAGTTAATTCAAGGAACTTCTGAGGAGTCCACTCTGTA
AAACAGCAGGTTAAATTCACTCAACCCATGTGGAAATTGATCTATATCTCTACTTCCAGGG
ACCATTGCCCTCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGATGCCACCAAG
GCTTCAGGAGTAGGGGAAGCCTGGAGGCCACTCCAGGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGTGTCCGGTGTACCTGC
TTCCATCTCCAGGCCACCAGCCCTGCCCACCTCACATGCCCTCCCATGGATTGGGCCT
CCCAGGCCACCTATGTCAACCTGCACTCTGTTCAAAATCAGGAAAGAAAAGAT
TTGAAGACCCCAAGTCTGTCAATAACTTGTGTGGAAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCAAAATTATTTGATGTATGAGTTGAGGTTG
TTTGTATATTAAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLRHYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEE
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSMDPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

FIGURE 23

CCAGAAGTCAAGGGCCCCGGCCTCCTGCCTGCCTGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCGGAAAGATGGCGAGGAGGAGCCACCGCCTCCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGCAAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAAAGAAACTGGGTGGAGTGTCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATAAAAATGTGACAAGAAGTGATGCCGGAAATATCGTTGTGAAGTTAGTGCCCCATCTG
AGCAAGGCCAAACCTGGAAAGAGGATAACAGTCACTCTGGAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAATCCAGCTCCTGAATAACACATGGTTAAGGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATAACACAATGAATACAAAAACTGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAATATTCCTGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCGGAAACGAATGCAAGTAGATGATCTCAACATAAGTGGCA
TCATAGCAGCGTAGTAGTTGTGGCCTAGTGATTCCGTTGTGGCCTGGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAGAAACCTCCTCCAGAAGAGTAATTCTCATCTAA
AGCCACGACAATGAGTGAAAATGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTGGAAAGG
CCGGCGGGCGGATACGGTCAGGAGTTCTAGACCAGTCTGGCAATATGGTGAAAACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAATCACTGAAACCCGGGAGGCGGAGGTTGCAGTGAGCTGAGATCACGC
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAAATAAAATAAAATAAATA
AATAAAATCTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATTC

FIGURE 24

MARRSRHRLLLLLLRLVVALGYHKAYGFSAPKDDQQVVTAVEYQEAILACKTPKTVSSRLE
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQGQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
RLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARNSGYRRCPGKRMQVDDLNISGIAAVVVA
LVI
SVCGLGVCYAQRKGYFSKETSFQKSNSSSKATTMSENVQWLTPV
IPALWKA
AAAGGSRGQEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAAACATGCTCCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCCCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCATCTATACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAAAGGAAATAGTAACCTCTCTCCAAATATGCATGACATTGGACAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTCATCA
TTGACAAATGCAAGCATCTCCTTATCAATCAGCTCCTATTGAACCTACTAGCACTGACTG
TGGAACTCTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCACTGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAG
TGGATTGTCCACGGTTATGTACGTGTGAAATCAGGCCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGTCTTTAACCTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCTCCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTTCCAGAAACCTTACTGGCCTGGATTATCTCAAAACAAATTATCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCCTGAAAAATGTCGTCCGAACGTGAGCAACTTACAAGAACTCTATATTAAATCACAACT
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTTCTCGACTTCATCTC
AATTCAAATAGATTGCGAGATGATCAACAGTAAGTGGTTGATGCTCTTCAAATCTAGAGAT
TCTGATGATTGGGGAAAATCCAATTATCAGAAATCAAAGACATGAACTTTAAGCCTTATCA
ATCTTCGCAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGCTTATTAAAGTACCCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCCTATTAAATAGAA
TACGAAGGGGTGATTTAGCAATATGCTACACTTAAAGAGTTGGGATAAAATAATATGCC
GAGCTGATTCCATCGATAGTCTTGCTGTGGATAACCTGCCAGATTAAAGAAAATAGAAC
TACTAACAAACCTAGATTGTCTTACATTCCCCAATGCATTTTCAAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCCTGTACCATGGTACCTGGTAC
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCATCAGGTGTACTGTGTACCGTTG
GATGAACATGAACAAACACATTGGATTATGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTTCAGGGACATGATGGAAATTG
CTCCCTCTTATAGCTCCTGAGAGCTTCTCTAATCTAAATGTTAGAAGCTGGAGCTATGT
TTCCTTCACTGTAGAGCTACTGCAGAACACCAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTGCTTAATACCCCTGACAGACAAGTTCTATGTCCTATTGAGGGAAACACTA
GATATAATGGCGTAACTCCCAAAGAAGGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGATCTTCCACAAGATAACAATG
GCTCTTGAATATTAAAATAAGAGATATTGAGCAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAATCTCAAATCTAGTAAATGGACAGCCTTGTCAAGACTGAAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCACCATCTACAGAAAAACAGAAAAAAA
TGTGTAAATGTCACCACCAAGGTTGCACCCCTGATCAAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCAATTAGGTGAGCTTATCCTCCTGTGATAAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCT
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMLPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRTSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNIAKIEYSTDTPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELSNLQELYINHNLLSTISPGAFIGLHNLLRLHLSNRQLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINRLSIVAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVVNLKFLLDKNPINRIRRGDFSNMLHLKELGINNMPPELISIDSIAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPEFQGQNRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSHAAQSARIPSDVKVVNLTHLNPKSTEYKICIDIPTIYQKNRKKCVNVTTKGLHPDQKE
YEKNNTTLLMACLGGLLGIIGVICLISPEMNCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

GCCCCGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGCTCGTATTATGCTGACATTCCAGC**ATGAATCT**
GGTAGACCTGTGGTTAACCGTTCCCTCCATGTGTCTCCTCCTACAAAGTTTGTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAACTGAGAGTTCTAACCTGTCCAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAATGCCTCAATAACCTGAAGGCCAGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTTGGCTGGTTCACTATGGTGTCTCATATGTGGTATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGT**ATAGTGT**CCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGTAAACACATTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACCTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTAACCTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDSNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLSDLSDNR
IQSVHKNAFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPF
LNAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCGCGCCGAGATGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCTGCTGGCAGCCCATCCTCTGCTGGTGCT
GGGCTCAGTGTGCTAGGCTCGGCCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGCCACCGCAAGTGTCTTGAGCAGTCCCCGAGGGCATCCCCACCGAG
ACGCGCCTGCTGGACCTAGGCAAGAACCGCATCAAAACGCTCAACCAGGACGAGTCGCCAG
CTTCCCGCACCTGGAGGAGCTGGAGCTCAACGAGAACATCGTGAGCGCCGTGGAGGCCGGCG
CCTTCAACAAACCTCTCAACCTCCGGACGCTGGGTCTCCGAGCAACCGCCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCCTCAGCAACCTGACCAAGCAGGACATCAGCAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCGCTTCAGCGGCCTCAACAGCCTGGAGCAGCTG
ACGCTGGAGAACATGCAACCTGACCTCCATCCCCACCGAGGGCGCTGTCCCACCTGCACGGCCT
CATCGCCTGAGGCTCCGGCACCTCAACATCAATGCCATCCGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCCTACTTGGACACCATGACACCCAAAC
TGCCTCTACGGCCTCAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGTTCTCAACCTCTCTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGGC
GGGCAGCTGGCGTGGTGGAGCCTATGCCTCCGGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAGTGACCACACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCCTGGACTCCAACCCGCTGGCCTGCGACTGTCGGCTCCTGTGGGTGTTCCGG
CGCCGCTGGCGCTCAACTCAACCGGCAGCAGCCCACGTGCGCCACGCCAGTTGTCAA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTCACCTGCCCGCG
CCCGCATCCGGGACCGAAGGCCAGCAGGTGTTGTGGACGAGGGCCACACGGTGCAGTT
GTGTGCCGGGCCGATGGCGACCGCCGCCATCCTCTGGCTCTCACCCCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGGCCACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCGCAGCTACTGCCGACTGCCCATCAGCCAAACAA
GACCTCGCTTTCATCTCAACCAGCCGGGAGGGAGAGGCCAACAGCACCGCGCCACTG
TGCCTTCCCTCGACATCAAGACCTCATCGCCACCACTGGCTTCACTCTTT
CTGGCGCTGCTCTCTGCTGGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACGCAGGCATCAGCTCCGCCG
ACGCCGGCGCAAGTTCAACATGAAGATGATATGAGGGCGGGCGGGGGCAGGGACCCCCG
GGCGGGCGGGCAGGGGAAGGGGCTGGTCGCCACCTGCTCACTCTCAGTCCTCCACCTC
CTCCCTACCCCTCTACACACAGTTCTCTCCCTCCGCCCTCCGCTCCCTGCTGCCCG
CCAGCCCTCACCAACCTGCCCTCTACAGGACCTCAGAAGCCCAGACCTGGGACCCCCA
CCTACACAGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTC
ATAATTCAATAAAAAGTTACGAACCTTCTGTAACTTGGTTCAATAATTATGGATT
TATGAAAACCTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPILLVLGSVLSGSATGCPPRCECSAQDRAVLCHRKCF
VAVPEGIPETRLLDLGKNRIKTLNQDEFASFPHLEELELNENIVSAVEPGAFNNLFNLRTL
GLRSNRLKLIPLGVFTGLSNLTKQDISENKIVILLDYMFDQDLYNLKSLEVGDNDLVYISHRA
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVLRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLA VRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLLIDSNPLA
CDCRLLWVFRRLWRLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV
FVDEGHTVQFVCRADGDPPIALWLSPRKHLVSAKSNGRLTVFPDGTLEVRYAQVQDNGTYL
CIAANAGGNDNSMPAHLHVRSYSPDWPHQPNKTFAFISNQPGEGEANSTRATVPFPFDIKTLI
IATTMGFISFLGVVLFCVLFLWSRGKGNTKHNIEIEYVPRKSDAGISSADAPRKFNMKMI

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCACAGCGTCCGACCTCGGCCCCGGCTCCGAAGCGGCTCGGGGGGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTGCCAGGCCAGCC
AGGGAGCCGGCGGGAAAGCGCGAGGGGCCCCAGCCGCTCGCTCCGCTCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCGGGGCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGCACCCTGGTGGCTCAAGTGCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCTGCTCAGCAGACTCTACTTGGGAGAAGA
GAGCCCTCGAGATAATCGAATTCACTGGTACCTCTACGCCAACGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTCACTATGCCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCCAATGGTAAAACCTTCACTGTCAGCAGCTCGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAAGCTGTTGCTACACTGTGAGGGTCGCGGCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAAGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGAACAGTGGCACCTACGGCTGCACAGCCACCAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCGGTGCCT
CCTCCTCCAGCACCTACCACGCCATCATCGTGGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCTTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCCAGACGGGACACGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTTCATTAGAGGCGCTGCCACTCCTGC
GCCCCCCAGGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCTGTACAGAATGTCTGC
TTTGGGTGCGGTTTGTACTCGGTTGGAATGGGAGGGAGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTGGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGGTGAGAAAAGCAAAAAACA
AACAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLKCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELSIISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNGK
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLLIMLIFLGHYLLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTTCTCCTTCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAAATTGTGCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGTTAAAAATGCTGCTTGGATTCTGTT
GCTGGAGACGTCTTTGCTGGAAACGTTACAGGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGACCTACACGTAGACTGTGAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCAATTATTCTGCATGGCAATT
CCTCACTCGACTTTCCATAATGAGTTGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTTGCATGAAATGTTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAAACAAGATCAAGTCTTTCGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTCTGCTCATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCTGCTAGAGGATAACCC
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCGAGTGGTCTGCGAAGCCCCCACCAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCCCGCTG
CCCAAGAAGAGACCTTGCTCCTGGACCCCTGCCACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGCAGCTGCGACCACATCCCAGGGTGGGTTAAAGATGAAC
TGCAACAAACAGGAACGTGAGCAGCTGGCTGATTGAAGCCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAGATCCACAGCATCCGAAAATCGCACTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAAATAACATCGCTACTGTAGAGAACACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACAGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTCAACAAACACTG
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCTTCAAGCAGTGGGCA
GAACGCTTGGGTTCCGAAGTGTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTCTT
TAGAAAGGATTTCATGCTCCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTGGCGAGACCGGACGCACCTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCTTCACCGTGGGGCATGCTCGTGTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACTCCTCCCGTCCGAGATTAATTCCCTACAGACAGTCTGT
GAECTTCTACTGGCACAATGGGCTTACACGAGATGGGCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTTAAGACCCCAACCCAAATAGGGAGGGCAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCCAAATCCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACAAACGAAAGGGCT
GACCCCTACTTAGCTCCCTCTTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGGCCCTTGTGAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATATCCACATCTATATAGAGAGATAGATATCTATTTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGCTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACTTGACTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCCKEKCSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNGLHEIVPGAFGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRDIDPGAFQDLNKLEVILINDNLISTLPANVFQYVPITHLDLRG
NRLKTLPLYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLPAPPQAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGTK
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCCNRNVSSLADLKP
KLSNVQELFLRDNKIHSIRKSHFDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNQIQLILPGTFNAMPKLRILILNNNLLRSLPVDVFAGVSL
SKLSLHNHYFMYLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFMLLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLL VFVTS AFTVVGMLV FILRN RKR SKR RDAN SASE IN SL QTV CDSSY WHNG PYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCCAGAATAACTCAGGGC
TGCACCGGGCTGGCAGCGCTCCGCACACATTCTCTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGATTCTTGGCAGTTGGGGGGTCCGTGGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCCAGACAC
AGCTCTGCGTCCTCGAGCGGGACAGATCCAAGTTGGGAGCAGCTGCGTGCCTGGGGCCTCAG
AGAATGAGGCCGGCGTTGCCCTGTGCCCTCTGGCAGGCGCTCTGGCCCGGGCCGGCGG
CGGCGAACACCCCCACTGCCGACCGTGTGGCTCGCTGCCCTGGGGCCTGCTACAGCCTGC
ACCAAGCTACCATGAAGCGGCAGGGCGCCGAGGAGGCCTGCATCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCGCTGTGCTCGCTCCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTCGACTGGAGCGCAGGCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCTCCGACCCCGGCGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCCTGCACCGCGGGAGATGCGC
GGTACTCCAGGCCACCGGTGGGTGAGCCCGCAGGCTGGAAGGAGATGCGATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCTGCCCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCCTGGAACCTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCGCAGAGCTCCCTAACTGCCTAGACGACTTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCCGCTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACGGGGTGCCACCAGGCGCCGGCCACT
GCAACCAGCCCCGTGCCGAGAGAACATGGCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCCTGAACAAGACAATTCAAGTAACTCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGTTACCCCTCAAATGTCCTCAAGCCGAGTCAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCCAAGTTAATTCTACGACTCCTCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGTCTTCATATTGTGAGCACAGCAGTAGTAGTGTGGTATCT
TGACCATGACAGTACTGGGCTTGTCAAGCTCTGCTTACGAAAGCCCTTCCAGCCA
AGGAAGGAGTCTATGGCCCGGGCTGGAGAGTGAACCTGAGCCGCTGCTTGGCTC
CAGTTCTGCACATTGCACAAACAATGGGTGAAAGTCGGGACTGTGATCTGCCGGACAGAG
CAGAGGGTGCCTGCTGGCGAGTCCCTTGGCTCTAGTGAATGCA**TAGGGAAACAGGGGA**
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACCTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGGAAAGTGCCTTAGGA
TGGTGAATCTGGGGACCGGGTAGTGTCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTGAACTTTCAAGACATTGAAACAAATAGAACACAATATAATTACA
TTAAAAAATAATTCTACCAAAATGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAAATAAAAATTAAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCPAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVLGLVKLCFHESPSSQPR
KESMGPPGLESDEPEPAALGSSAHCTNNGVKVGDCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATTCAAGCAGTGGCTGTGGCTGCCAGAGCAGCTCCTCAGGGGAAACTAAG
CGTCGAGTCAGACGGCACCATATAATCGCTTAAAGTCGCTCCGCCCTGCCGGCGCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGGGTGCAGCGCTGAGAGAGGGAGCGCGCGGGCAGCCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGGTGTGAGCGCGGGTGGTGCAGA
GGGGCGTGTGTGCCGGCGCGCGCCGGTGGGTGCAAACCCCGAGCGTCTACGCTGCCATGA
GGGGCGCGAACGCCCTGGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCGG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGGCATTCTTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTTGAAAATCA
CAGTTCCCAGAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGGCCATGCCAATGCCAGCGCATTGGCCG
CTTCTGTGGCCTTCCGGCTGGAGCCCTGTGTCCAGTGGCAACAAGATGATGGTGCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACCGGGATTACCGTCACTGTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGTAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACTTCTTATTCACT
TTTATCAGACTTAAGTTAATGCACTGGGTTATTGGTCACTACATATTCAAGGCCAAA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGGTTAAA
ACCCACCGTGGCCTGTGTCAACAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGACTTTGTATTAGCCGGCACTGTTATCACAACCACACTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCGATTCAAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGTGCAAGCAGTGCCTCTCCTCAGAACAGGTC
TAAATTACATTATTATGGGCAAGTAGGTGAAGATGGGAGGGAAAATCATGCCAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCTCCTGGATGCCCTAAAAAATAAGCAATG
TTAACAGTGAACGTGTCCATTAAAGCTGTATTCTGCCATTGCCCTTGAAAGATCTATGTT
TCTCAGTAGAAAAAAATACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GACTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGGAAAGTTCTT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCGACTTAGTGCAGGTGATAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATTTATACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGTGAAGATGTCAAAAAAAAGATTTAGAAGTGAATATTATAGT
GTTATTGTTCAACCTCAAGCCTTGCCTGAGGTGTTACAATCTGTCTTGCCTTCTA
AATCAATGCTTAATAAAATTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYVAVFNGGEVNDARRIGKYCGDSPPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMGQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCGCGGGCTGGGGCGGTGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACCTTGGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCTGC
CTTCCCTGTCTGGGGAACAGAGAGGCCCTGCCGTGGCTACGGCAGTGTGAAGGAGAACGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAATGTTGCAATGCAAGAACGG
CTGGCCCTGCATCACCTCAAGTGTAGACATTGATGAGTGAGTGACAGAGGCCAACT
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTCGATGTGGATGAGTGTGAGACAGAGGTGTGCCCCAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCCAGAGTCAGCAGGCTTCTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTTCACCGCCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCAGTGGCAGGCTGGAGGGCTCATCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTTGGTTATTTGAGAGTGGGTAAGCACCCCTACCTG
CCTTACAGAGCAGCCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTCTCACCTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSKSDFECHRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPCCPGTERPCGGYGCCEGEGTRGGSGHCDCQAG
YGGECAGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNCLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMGAGPGRCKKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTGCTCCTCCAGGGCA
GCACCATGCAGCCCCCTGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGAGCTCAAAGAGGT
GCCCACCTGGACAGGGCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGACCGCTCCCGCGAAAGAGGTTAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGGTCTGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCCTTCCAGG
AGCCGGTCCCCAAGGCCGCGCTGCACAGGCACGGCGCTGTCCCCGCGCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTCGCGTCCCGACAGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCCTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCCCTCGCAGGGGGC
GCCAGCCGGCTTGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTTGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGCCGAGAACTGGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGGCACCTGCCGGCAGCCCCCGGAGGCCCTGGCCTCAAGTGGC
CGTTCTGGGGCCTCGACAGTCATCGCCTCGGAGACTGACTCGCTGCCATGATCGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCAAGGAGGCTCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTGCAGGGTACCAAGGAGAGCTG
GCGATGACTGAACGTGCTGATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTATTCTATTACTGCACTATATTCTAACGCACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTTGTCTGTAC
TGGATCTGGCTAAAGTCCTCCACCACCACTCTGGACCTAACGACCTGGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGAAAACATGAATAAAACACATTATTCT
AAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFSREVAGRFLALEASTHLLVFGMEQRLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLRVRDDGSNRTSLIDSRLVSVHESGWKAFDVTEAVNF
WQQLSRPRQPLLLQSVQREHLGPLASGAHKLIVRFASQGAPAGLGEQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWP
LGPRQCIASETDSLPMIVSIKEGGRTRPQVVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

FIGURE 43

GTCTGTTCCAGGAGTCCTCGCGGCTGTTGTCAGTGGCCTGATCGCGATGGGACAAA
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACCTCTGAACCTGAAGTCAGAATTCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAGTTGACCA
AGGAGACACCAACCAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTTGCCAACGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC
ACTTGTATGGTCTCTGAGGAAGGCGAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGGAACCGGG
CAGTGCTGACATGCTCAGAACAGATGGTCCCCACCTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCCTCAGCAACTCTCCTATGTCT
GAATCCCACACAGGAGAGCTGGTCTTGATCCCCTGTGAGCCTCTGATAACTGGAGAACACA
GCTGTGAGGCACGGAATGGGTATGGGACACCCATGACTTCAAATGCTGTGCGATGGAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCCCTGATTCTCCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCCGAAGTGAAGGAGAACCAAACAG
ACCTCGTCATTCTGGTGTGAGCCTGGTCGGCTCACCGCCTATCATCTGCATTGCCTTACT
CAGGTGCTACGGACTCTGGCCCTGATGTCTGTAGTTCACAGGATGCCATTGTCTTC
TACACCCCACAGGGCCCCCTACTTCTCGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTGCGAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTGGTTCTGGCTCTTCCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCTTCCATCTCTGGGCCACTCTCTGTCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCCCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTAAAACCGCTGCTAAAGAAAAGAAAAGCTGGAGGCTGGCGCAGTGGCTACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTTGGATCAGCCTGACCA
ACATGGAGAACCCACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCGTAGTC
CCAGCTGCTCAGGAGCCTGGCAACAGAGCAAAACTCCAGCTAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPVKLSCAYSGFSSPRVEW
KFDQGDTTRLVCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPSEYTWFKDGIVMPTNPKSTRAFSNS
SYVLNPTTGEVLFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGCTGTGGGACAGC**ATG**AGCGGCGTTGGATGGCGCAGGTTGGA
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCGCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGACCAAGTGGCTTATGCGTGCCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCAACACTGCCTATGGGTTATTGCAGCTGCTGCCGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCCTTGTCCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAACAGAC
CTCGCTGCC**TGAGG**ACAAGCAGTGGCACCACCGTCACTCAGCCCTGGCGTAGCCGGACA
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACAGAC
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCRDLDSDGSDEEECRIEPCTQKGQCPPPPGLPCPCTGVSDCSGGTDKKL
RNCSRLLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELGCGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

CCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCGGCGGAGCAGAGGTCGCGCACAGATGCGG
GTTAGACTGGGGGGGAGGAGGAGGAGGAAGGAAGCTGCATGCATGAGACCCACAGA
CTCTTGAAGCTGGATGCCCTCTGTGGATGAAAGATGTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTG
GCCGTGATCCTGTGGTTCAGCTGGCCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTCAAGTGTGCTGACCCGGCATTCCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAATCATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTATGTCGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCGTGAGACCTCTAGCCTCTTCTAATGGCTATGTAAACATCTCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGGCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCTGCT
GCCACCCGGCCTTGTGAGCGCTACAACCACGGAACGTGGTGAGTTACTGCGATCCT
GGCTACAGCCTCACCAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGGTTCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGGTGCTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCTCCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTCCCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGGCTTGAGTGCCTTAGGCCCGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCCGTGGACGACCAGAGCCCCCAGCATAACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCCACCTGCTCGGACAACCTGACATA
ATTGCCAGCAGGAGGGAGGTGGCATCCACCAGCCAGGCATCCATGCCACTGGGT
GTTGTTCTAAGAAATGATTGATTAAAAAATTCCAAAGTGCCTGAAGTGTCTTCAA
ATACATGTTGATCTGTGGAGTTGATTCTTCTCTTGTGAGGTTAGACAAATGTAAACAA
AGCTCTGATCCTAAAATTGCTATGCTGATAGAGTGGTGAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTAAAATTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQQQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHQCQDGFKLKGA
T KRLCLKHFN
GTGWI
PSDNSICVQEDCRI
PQIEDAEIH
NKTYRHGEKLI
ITCHEGFKIRY
PDLHN
MVSLCRDDGT
WNNLPI
CQGCLRPLAS
SNGYVN
ISELQ
TSFPV
GTVISY
RCFP
GFKLDG
SAYLE
CLQNL
IW
WSSPPR
CLALEA
QVCPLP
PMVSH
GDFV
CHPR
PCERY
NHGT
VVEFY
CDPGY
SLTSDY
KYITC
QYGEW
FPSYQ
VYCIK
SEQT
WPST
THE
TLL
TTW
KIV
AFT
ATSV
LLV
LLV
IL
ARM
FQT
KFK
AH
FPP
PR
P
RSS
SSD
PDF
VV
VD
GVP
VML
PSY
DEA
VSG
GLS
ALG
PGY
MAS
VGQ
GCPL
PVDD
QSPP
AYPG
SGD
TDT
GP
GE
SET
CDS
VSG
SSELL
QSL
YSPP
RCQ
EST
HP
PAS
DNP
DII
IA
STA
EE
V
AST
SPGI
IHH
AH
WVL
FLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACCGCGTCCGCTCCGCGCCCTCCCCCCCCTCCCGTGCAGTCCGTCCGTGGCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTCGCGCACGCCCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTCCGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAAACCGCGCTACAGG
CCGTGCTGCCGTGCTGGTGGGCTGCCGCCAGGGTCGCCTGCTGAGTGC
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTGTTA
TAAAGTCATTACTTCATGATACTTCTCGAAGACTGAACATTGAGGAAGCAAAGAACCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATTGAAAACCTCTGCCATCTGATGGTGAACCTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTGGACTGATGGCAGCATAT
ACAATTTAGGAACGGTATGTGGATGAGCCGTCCTGCCAGCGAGGTCTGCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACAAATTCTATTGCAAATATTCTGATGAGAAACCAGCAGTCCTT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACAGCTGCCCTGAATCTGGCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTGTGGTACCAACAGTTGTATGTTGGTTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCCCTAGCACAAAGAACACACCATC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGCCAGACCTGAAGAAATATTCTATTCCGAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTTGTGACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGAGCGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGAAATGAAATATATG
GTTATTAGGACATATAAAAACGAAACTGACAACATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGAAAATACACAGAACGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCCTGGACCCCCACGTTGGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAACGGTACCTTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCACTTGGTTGGTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGCTGTGGAGCTTGGAAAACCACCTCTGTTTCCCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAACATTCAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATCGGAATTCTCATATCTGTTTTCAAAGAACAAATCAAATAAAGA
GCAGGAAAAAAA

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRGGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIKEFIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLLLV
VTTVVCWVWICRKRKREQPDPSTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSCGEATPDDMSCDYDNMAVNPSSEGFTVLSVESGFVTNDIYEFSQDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTTGTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCGCTGAGCCCCGGCGCCGCAGAAGACTTGT
GTTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATACTGGTGT
GTTCA
GTCAGCATGCCTGTGGACCCCAGTGGCGTCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGCCAGTGTCCGGTCACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGCGTTGACACGGGGCTCGGAGTCCTCTCAAGCC
GCTCCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCATT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGAAGACATTCCCTTTC
TTTCACCAACCTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCA
GAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTCA
GAGAAGTCTTGTATCCAACTACCAAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTGATAAAGTGGACTTCTTCATCCTCCT
GGACAACGTGGCTGCCAGCAGGCACACAACCTCCAAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACCA
GAGCAGCTGGAAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCA
GGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTTAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHNLPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCP LDMLNAMS VYTLSPEKYHALCSQTQVMEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC GGCTGGTGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGGACCCTGTGTGATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGTCTCATCCA
ATCAGTCAGTTGCACAGGAACAGAACAGATACTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTCTTCTCCCCA
GTCCCAGAGGGTGTCAAGGCTGGCTGACGCCCTGGCATTGCAAGGGACGCGTGGAAAGTGAA
GCACCAGAACCAAGTGGTATACCGTGTGCCAGACAGGCTGGAGCCTCCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCCTCA
GGATTGCCCTCTGGCCTTGGGAAAGAACACCTGCAACCATGATGAAGACACGTGGTCTG
AATGTGAAGATCCCTTGACTTGAGACTAGTAGGAGGAGACAACCTCTGCTCTGGCGACTG
GAGGTGCTGACAAGGGCGTATGGGCTCTGTGTGATGACAACGGGAGAAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGGAAGTCCCTCTCCCTCAGAGACCGGA
AATGCTATGCCCTGGGTTGGCCGATCTGGCTGGATAATGTCGTTGCTCAGGGAGGAG
CAGTCCCTGGAGCAGTGCCAGCACAGATTTGGGGTTTCAGCACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGCATCATCTAATCTGTTGAGTGCCTGAATAGAA
GAAAAACACAGAAGAAGGGAGCATTACTGTCTACATGACTGCATGGATGAACACTGATCT
TCTTCTGCCCTGGACTGGACTTATACTTGGTGCCTGATTCTCAGGCCTCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCCATCAGACATAGTTGGAACATACATCA
CCACCTTCCTATGTCACATTGCACACAGCAGATTCCCAGCCTCCATAATTGTGTGTAT
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACACACATA
CACCAATTGTCCTGTTCTCTGAAGAACTCTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAACGGAATTAAAGGATAAATTCTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAACTTATTACAATAATAAGATAGCAC
TATGTGTTAAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWVECEDPFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRILW
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTGACCTCGAC
CCACCGCGTCCCGGGACCGTGGCGGACCGTGGGCCGGTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTCTTCCGGCTGCTGCAGTGGGTGCGCGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCACCTCAGGGCTGGCAAAGAATGTGAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTTCTCATGCCACCAAGGTGCAGACACACAAGCCTACTTGGTGACCTTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGCTATGTC
GACATACTTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACCAAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGGAGGAAGGCCACATTGTCGCCATCAGCAGCATCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGAA
CTGTCTCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCAGGATGGATCTAGGTATGGAGTTATGGAC
ACCACACAGCCCAGGGCGAAGCCCTGTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTTCTGGCTGTTATCTCGAA
CTCTGGCTCTGGCTCTTCAGCCTCATGGCCTCCAGGGCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAAGCAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGAGACTTTAATGGAGATTGCTCACAAGTGG
AAAGACTGAAGAACACATCTCGTGAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTCCCAGGGTGAGGGAAACACTTAAGGAATAATATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAGGGCGGCCGCGACTCTAG
AGTCGACCTGCAGAAGCTTGGCCGCCATGGCCCAACTTGTATTGCAGCTTATAATGGTTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLQQWVRGKAYLRNAVVIITGATSGLGKECAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAIVAAAAEILQCFGYVDIL
VNNAGISYRGTIMDTTVVDKRVMETNYFGPVALTKALLPSMIKRRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLAAGKKKDVILADLLPSLAVYLRTLAPGLFFSLMASRARKERKSKNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGATGAAATTCTTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGCTGATTACAGGAGCTGGCATGGAATTGGGA
GACTGACTGCCTATGAATTGCTAAACTAAAAGCAAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGACTGGTGCCAGGTTACACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGCACATTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATGGCCATATTGTCAGTGTGGCTCGGCAG
CTGGACATGTCTCGGTCCCCTCTTACTGGCTACTGTTCAAGCAAGTTGCTGTTGGA
TTTCATAAAACTTGACAGATGAAGTGGCTGCCTAACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTAATTCGTAAACACTGGCTTCATAAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTTT
CCTGGCAGTTTAAAACGAAAAACTCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAGCACCTAGTTCTGAAAAGTGAATTACAGGTTAGGTTGATGTCATCTA
ATAGTGCCAGAATTTAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTAAGGAAATGAAGAAAAAGAA
CCAAAATGACTTTATTAAAATAATTCCAAGATTATTGTTGACTTAAATTGTTG
AATTGTACCATACCGTTATTAAACATATATTATTATTGTTGATTGACTTAAATTGTTG
ATAATTGTGTTCTTTCTGTTCTACATAAAACTCAGAAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTCAACATGAATATCATGAACTCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCCCTGAGAGATACCTCACATTCAATGCCAACATTCT
GCACAGGGAAGCTAGAGGTGGATACACGTGTTGCAAGTATAAAAGCATCACTGGGATTAAAG
GAGAATTGAGAGAATGTACCCACAAATGGCAGCAATAATAAATGGATCACACTTAAAAAAA
AA
AA

FIGURE 58

MKFLLDILLPLLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAAKCKGLGAKVHTFVVDCSNREDIYSSAKVKAEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

FIGURE 59

CCACCGCGTCCGGACCGTGGTCGACTAGTTAGATCGCGAGCGGCCGCCGCGCTC
AGGGAGGAGCACCGACTCGCCGCACCTGAGAGA**ATGGTGGTGCCTAGTGGAAAGGTGATTG**
TTTCGCTGGTCCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATACAGAAGT
GTTCCATGCCACCTAACGGAGACTCAGGACAGCATTATTCTCACCCCTTACATTGAAGC
TGGGAAGATCCAAAAGGAAGAGAATTGAGTTGGTGGCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTGGCTACAGGGTGGGCCGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCCTATGTTGTCACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGCTTCAGTTTACTGATGATAACCCACGGATATGCAGTCATGAGGACGATGT
AGCACGGGATTATACAGTCATAATTCAAGTTCCAGATATTCTGAATATAAAAATA
ATGACTTTATGTCACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCTGTGAGAGAGGTGAAGATCAACCTGAACGGAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTTGGATGAGAACAAAAAGTACTCCAGAACAGCAGTGCCTGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAAATACTGGATAAAACTACTAGATGGCACTTAAC
AAGTGATCCTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGAAATTGTCACTCCAGAGGTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGAAACTATAGTGAAGTACTTGCAGA
AGATACAGTACAGTCAGTTAACGCACTGGTAACATGAAATCATGAATAATTAAAGGTTCTGA
TCTACAATGCCAACACTGGACATCATCGTGGCAGCTGCCCTGACAGAGCGCTCCTGATGGC
ATGGACTGGAAAGGATCCCAGGAATACAAGAAGGCAGAAAAAAAGTTGGAAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTCCATCAGGTAATTATC
GAGGTGGAGGACATATTTACCCATGACCAGCCTCTGAGAGCTTGACATGATTAATCGA
TTCATTTATGGAAAAGGATGGATCCTTATGTTGATA**AAACTACCTCCAAAAGAGAACAT**
CAGAGGTTTCATTGCTGAAAAGAAAATCGAAAAACAGAAAATGTCATAGGAATAAAAAAA
TTATCTTTCATATCTGCAAGATTTCATCAATAAAATTATCCTGAAACAAGTGAGC
TTTGTGTTGGGGGAGATGTTACTACAAATTAAACATGAGTACATGAGTAAGAATTACA
TTATTTAACTAAAGGATGAAAGGTATGGATGATGTGACACTGAGACAAAGATGTATAATGA
AATTAGGGTCTGAAATAGGAAGTTAATTCTCTAAGAGTAAGTGAAAAGTGCAGTTG
TAACAAACAAAGCTGTAACATCTTCTGCCAATAACAGAAGTTGGCATGCCGTGAAGGT
GTTTGGAAATATTATGGATAAGAATAGCTCAATTATCCAAATAATGGATGAAGCTATAA
TAGTTTGGGAAAAGATTCTCAAATGTATAAAGTCTTAGAACAAAAGAACATTCTTGAAATA
AAAATATTATATAAAAGTAAAAAA

FIGURE 60

MVGAMWKVIVSLVLLMPGPCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGRELSL
VGPPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTSNMTLRDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHЛИHSLNPVREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFQAFEILDKLLDGDLTSDPSYFQNVTG
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHVGQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEKVWKIFKSDSEVAGYIRQ
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT
TTTCCCTTCTAACAAAGTCTAACAGCTGTTCAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTGACCAGCTCCTT
CCTCTCTGTGGATAACAGAGCATGAGAAAGTGAAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCCTAACAAAGCTTCAAAAAACAGGAGCAGCTCCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCCTAACATATCAAATTGACTGGCTGGG
TGAACATTCAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTAACGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAATTAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAAACAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCCAGGATGGGACCCCTGGGTC
AGGCCAGCCTTTGCTCCTCCGGAAATTATTGGTCTGACCACTGCCTTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCAGTGGTCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCCTCAGTCAGCACCTTCACTCTGAGAATCGTGAUTGGACCTTCAACCACCTGACCGT
CCACCAAGGGACGGGGCCGTCTATGGGGGCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCCG
CCCTCATCGTGCAGCCCTGAGCGAAGTGCTCACCCCTACCAACAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGAGCCTCTACCAGGGGTCTGCA
AGCTGCTGCCGCTGGATGACCTCTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTCTTATCGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCGAGA
CCCTGAGGGTGTGCCATCAACTCCGCTGGAGACCTCTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCAAAGTCCACTCATACGTGCCCTGCCCTGGCTGCACCCGGC
CGGGTGGAAATACCGCCTCTGCAGGCTGCTACCTGCCAACGCTGGGACTCACTGGCC
AGGCCTTCAATATCACCAAGCCAGGACGATGTACTCTTGCCATCTTCTCAAAGGGCAGAAG
CAGTATCACCAACCGCCCGATGACTCTGCCCTGTGCTGCCCTCCATCCGGGCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGG
TGCTGGGAAGGACGTCCAGTGCACGAAGGCGCTGCCCCATCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGAGGCTCAACTCCAGTGGAGGGCCTGACCCGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGCCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGCTGAAAAAGGTAAGAGTCTATGAGTTGAGCTCAATGCC
ATTCACCTCTCAGCAAAGAGTCCCTTTGGAGGCTAAGGTAGCTATTGGTGGAGATTTAACTATAG
GCAACTTATTTCTGGGAACAAAGGTGAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTTCTAGCTACTTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLGNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFLILVEPSHKKEHYLSSVNKTGTMGVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLPRDPESSAMLDYELHSDFVSSLIKIIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFHYSVSLPFGCTRAGVEYRLLQAAYLAKP
GDSLAQAFNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEGN
LELNWLLGKDVQCTKAPVPIDDNFCGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTSGKLKKVRVYEFRCSNAIHLLSKESLLEGSYWWRFNYRQLYFLGEQR

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGCGGCTGAGTGGACTGGAGTGGAAACCCGGGCCCCCGCTTAGAGAACACCGCGATGACCA
CGTGGAGCCTCCGGCGGAGGCCGGCCCGCACGCTGGACTCTGCTGCTGGCTCTGGGCTTCTGGTGCCTCC
GCAGGCTGGACTGGAGCACCCCTGGTCCCTCTGCGGCTCCGACATCGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTCGGGGCTCCATCCACTATTTCCGTGTGCCAGGGAGTACT
GGAGGGACCGCTGCTGAAGATGAAGGCCTGGCTTGAAACACCCACCAACCTATGTTCCGTGGAACCTGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGGAACCTGGACCTGGAGGCTTCGTCCTGATGGCCGAGAGATCG
GGCTGTGGGTGATTCTGCGTCCAGGCCCTACATCTGCACTGAGATGGACCTCGGGGCTTGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGGGCTGAGGACAACCTACAAGGGCTCACCGAAGCAGTGGACCTTATTGACCA
TGATGTCAGGGTGGTGGCACTTCAAGCGTGGGGACCTATCATTGCGTGCAAGGTGGAGAATGAATATG
GTTCTATAATAAAAGACCCGCATACATGCCCTACGTCAAGAAGGCACTGGAGGACCGTGGCATTGTGGAACCTGC
TCCTGACTTCAGACAACAAGGATGGCTGAGCAAGGGGATTGTCCAGGGACTCTGGCCACCATCAACTTGCACT
CAACACACGAGCTGCAGCTACTGACCACCTTCTCTCAACGTCAGGGACTCAGGCCAAGATGGTGTGAGT
ACTGGACGGGGTGGTTGACTCGTGGGAGGCCCTACAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCAATTGAGCAGCCGCTCCATCAACCTCTACATGTTCCACGGAGGACCAACTTGGCTTCAATGAATG
GAGCCATGCACTCCATGACTACAAGTCAGATGTCACCGAGCTATGACTATGATGCTGTGACAGAACGGCG
ATTACACGGCCAAGTACATGAAGCTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCTCCCTCCCCACCTG
ACCTCTTCCCAAGATGCCGTAGGCCCTAACGCCAGTCTGTACCTGCTCTGTGGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGAAATGGACAGTCC
TCGGGTACATTCTCTATGAGACCAGCATCACCTCGTCTGGCATCCTCAGTGGCCACGTGATGAGGGGCA
TGTTGTGAACACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATGCTGTCCCCCTGATCCAGGGTT
ACACCGTGTGAGGATCTGGTGGAGAATCGTGGCGAGTCAACTATGGGAGAATATTGATGACCAAGCGCAA
GCTTAATTGAAATCTCTATCTGAATGATTCAACCCCTGAAAAACTTCAGAATCTATAGCCTGGATATGAAGAAGA
GCTTCTTCAGAGGTTGCCCTGGACAAATGGNNTTCCCTCCAGAAACACCCACATTACCTGCTTCTTCTGG
GTAGCTTGTCCATCAGCTCCACGCCTTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA
TCAATGGCCAGAACCTTGAGCGTACTGGAACATTGGACCCAGAAGACGCTTACCTCCAGGTCCCTGGTTGA
GCAGCGGAATCAACCAGGTACCGTTTGAGGAGACGATGGCGGCCCTGCATTACAGTTCACGGAAACCCCC
ACCTGGGAGGAACCAAGTACATTAAGTGAGCGGTGGCACCCCTCTGCTGGTGCCTGGGAGACTGCCGCTC
CTCTTGACCTGAAGCCTGGCTGCTGCCACCCCTCACTGCAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGGCTACAGTCTGCCCTGTCTAGCTCAAAACCTAAGCTGCAGGAAAGGTGGATGGCTCTGGGCC
TGGCTTGTGATGATGGCTTCTCAAGCCCTGCTTGTGCGAGGCTGTGGCTCTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCCTCAGAAAAAGTGTGAAACGTCGCCCTTGACCCGACGTACAGCCC
TGCAGCATCTGCTGGACTCAGCGTGCTCTTGCTGGTCTGGCCACATCCCTCATGGCCCCCAT
TTTATCCCCGAATCCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAAGGGGTGTCTCACCTGAGCTGACTTTGTT
CTTCCCTCACACCTCTGAGCCTTCTGGATTCTGAAGGAACCTGGCTGAGAAACATGTGACTTCCCC
TCCCTCCCACTCGCTGCTCCACAGGGTGACAGGCTGGGCTGGAGAACAGAAATCTCACCTGCGTCTTCC
CAAGTTAGCAGGTGCTCTGGTGTTCAGTGAGGAGGACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
CATCCAGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
AGGGAGGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
GGAGGACAGAAGGCCAGCTCACATGTGAGTCCTGGCAGAAGCCATGGCCATGTCTGCA
ACAGAAGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCACGCCAACAGCAGGGCAGAGCAGCCCTCCTTC
GAAGTGTGTCAGTCCGATTGAGCCTTGTCTGGGGCCAGCCAACACCTGGCTTGGCTACTGCTCTGA
GTTGCAGTAAAGCTATAACCTGAATCACAA

FIGURE 64

MTTWSLRRR PARTL GLLL VVLGFLV LRR LDWSTL VPL RL R H R Q L G L Q A K G W N F M L E D S T F W
I F G G S I H Y F R V P R E Y W R D R L L K M K A C G L N T L T T Y V P W N L H E P E R G K F D F S G N L D L E A F V L M A
A E I G L W V I L R P G P Y I C S E M D L G G L P S W L L Q D P G M R L R T T Y K G F T E A V D L Y F D H L M S R V V P L Q
Y K R G G P I I A V Q V E N E Y G S Y N K D P A Y M P Y V K K A L E D R G I V E L L L T S D N K D G L S K G I V Q G V L A T
I N L Q S T H E L Q L L T T F L F N V Q G T Q P K M V M E Y W T G W F D S W G G P H N I L D S S E V L K T V S A I V D A G S
S I N L Y M F H G G T N F G F M N G A M H F H D Y K S D V T S Y D Y D A V L T E A G D Y T A K Y M K L R D F F G S I S G I P
L P P P P D L L P K M P Y E P L T P V L Y L S L W D A L K Y L G E P I K S E K P I N M E N L P V N G G N G Q S F G Y I L Y E
T S I T S S G I L S G H V H D R G Q V F V N T V S I G F L D Y K T T K I A V P L I Q G Y T V L R I L V E N R G R V N Y G E N
I D D Q R K G L I G N L Y L N D S P L K N F R I Y S L D M K K S F F Q R F G L D K W X S L P E T P T L P A F F L G S L S I S
S T P C D T F L K L E G W E K G V V F I N G Q N L G R Y W N I G P Q K T L Y L P G P W L S S G I N Q V I V F E E T M A G P A
L Q F T E T P H L G R N Q Y I K

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGTCCAGGACC
CTGGTGAGGGTTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAGCCGGCTCGGCCGAGGCCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCT
AAGAAGCTGTCTGCCCTCGTCCCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTCGTAGTGGATAGGGGTATGACCGGTTCTCTAGACGGGGCC
CGTCCGCTATGTGTCTGGCAGCCTGCACTACTTCGGTACCGGGTACCGGGTCTTGGGCCAC
CGGCTTTGAAGATGCGATGGAGCGGCCTCAACGCCATACAGTTATGTGCCCTGGAACTA
CCACGAGCCACAGCCTGGGGTCTATAACTTTAATGGCAGCCGGACCTCATTGCCCTTCTGA
ATGAGGCAGCTCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGCAGAG
TGGGAGATGGGGGTCTCCCATCCTGGTTGCTCGAAAACCTGAAATTCATCTAAGAACCTC
AGATCCAGACTCCTGCCGAGTGGACTCCTGGTTCAAGGTCTGCTGCCCAAGATATATC
CATGGCTTATCACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGTGGCTCTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GA^{CT}CTATACCAC^TGATTTGGCCCAGCTGACAACATGACCAAAATCTTACCC^TGCTT
CGGAAGTATGAACCCCATGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATTA
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCATAAGAAGGGACGCTCCTCCGATTACTACCAGCTATGACTATGATGCACC
TATATCTGAAGCAGGGGACCCACACCTAACGCTTTGCTCTGGAGATGTCATCAGCAAGT
TCCAGGAAGTTCCCTGGACCTTACCTCCCCGAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTTGGCATTACTGGCTTCCTAGACTTGCTTGCCTTGGCCCGTGGCCCAT
TCATTCAATCTGCCAATGACCTTGGAGGCTGTCAAGCAGGACCATGGCTCATGTTGTACC
GAACCTATATGACCCATACCATTGGAGCCAACACCATTCTGGTGCCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGTCCAAACTGGATATCTGGTGAGAACATGG
GGAGGCTCAGCTTGGCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCCTACCCAGTGGATGATGTTCCCTGAAAATTGATAACCTTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGCCATATCCTCAAGCTCTCTGGCCCCACATTCT
ACTCCAAAACATTCCAATTAGGCTCAGTTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCCAAGTCTGGATCAATGGTTAACCTGGCCGTA^TGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGCACTGAAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCAGTGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTAAACCCCGTCTCCACTAAAAATACAAAAATTAGCCGGCGTG
ATGGTGGGCACCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTGAATCC
AGGAGGCAGAGGTTGCAGTGAGTGGAGGTTGTACCACTGCACTCCAGCCTGGCTGACAGTG
GACACTCCATCTCAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLTLLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFKVLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPHGPLVNSEYYTGWLWQNHSTRSAVTKGLENMLKLGASVNMYMFHGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPGLPPPSPKMMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMTHTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTIILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSAADTLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAAGCTTCTCATCAGTTACATATCCATTATTTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAAGGATACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAAACGATTT
GCGTCCTCTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTGGTGTGTT
CTTGTCAAGAAGTTAGTGAAAATAACTTAGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCCCTGCCTGGGTGTATTGCTCAAAAA
CCTTCGAGAGTTGTACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTTACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTCTAACATTACAGGAACGGAT
TTAAAGTCCAATAACATTGCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAAATTATGGCATAACAAAATTGTTACTATTCCCTCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCTAACACAACAGCTCGAACCTTACCAAGTGGAGTATT
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAACAAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCAGCTGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCTGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTTAAACTAAGATAATATATGACAGTGTGAGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGTAGGGTTTAAGTCATTCAACATTCAAGTAAATCTTTTTTTCTTTGGGG
AAAGGGAAGGAAAATTATAACTAAATCTGGTTCTTTAAATTGTTGTAACCTGGAT
GCTGCCGCTACTGAATGTTACAAATTGCTTGCCTGCTAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLQRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPAKEKIPAKISQMTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAWVYLLKNLRELYLIGNLNSENNKMICLSELRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIIISFQHLKRLTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCNDRLPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355, 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCAACGGCGTCCGGCCTTCTCTGGACTTGCATTCCATTCCCTTTCATTGACAAACTGACTTTTTATTCT
TTTTTTCCATCTCTGGGCCAGCTGGGATCCTAGGCCGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGGTTTCTTCTTCCCTCCCTGACATTGGCATTGCTTAGTGGTTGTGTTGGGGAGGGAGACCACGTGG
GCTCAGTGCCTGCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGCACCTCCATACAGTGAATTATGCCTGTC
ATCGCTGGTGGTACCTCTGGCGGCTTGCTCTGCTGATAGTGTGCTGCTCTGCTTTACTTCAAAATACACAAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGGCTGTAAGGAAACCCAGACAAGGTGTGGGGCAAG
AACAGCCAGGCCAAACCAATTGCCACGGAGCTGTGCTGCCCTGCAAGTGAGGATATAGAATGTGTGCC
AGTTTGATTCCCTGCCACCTTGCTGCGACATAATGAGGGCCTCTGAGTTAGGAAAGGCTCCCTCTCAAA
GCAGAGCCCTGAAGACTTCAATGATGTCATGAGGCCACCTGTTGTGATGTGCAGGCACAGAAGAAAGGCCAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGGAACCGAGCTGCTGGAGATCCCTACAGAGAGCTC
CACTGGGGCAACCCCTCAGGAAGGAGTTGGGGAGAGAGAACCCACTGTTGGGAATGCTGATAAAACAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGCTGAACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGCCAAAATGGAGCTTGTA
AGAAGGCTCATGCCATTGACCCCTTAATTCTCCTGTTGGCGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGCACATGGCAGAGACCCACAAAGCCATGATCCTGCAACTCAATCCC
AGTGAGAACTGCACCTGGACAATAGAAAGACAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGTGAAAGTGAACATTAAAGTCTTGACGGAACCTCCAGCAATGGGCCTGCTAGGG
CAAGTCTGCAAGAAAAAGCACTATGTCCTGATTTGAATCATCATCCAGTACATTGACGTTCAAATAGTTACT
GAECTCAGCAAGAATTCAAAGAACTGCTTTGCTCTACTACTTCTCTCTCTAACATCTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGAGGATCCTCACAGGCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTGTCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTTCAAGAGATTTCTAGAAATAGAC
AAACAGTGCACAAATTGATTTCTGCCATCTATGATGGCCCTCACCACACTCTGGCTGATTGGACAAGTCTGT
GGCCGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGCTACAGATTATGCCAAATTCT
TACGGGGATTCTGCTCCTACACCTCAATTATGAGAAAACATCAACACTACATCTTAACTTGCTCTCT
GACAGGATGAGGTTATTATAAGCAACCTCACCTAGAGGTTAACTCTAACTGGAAATAACTTGCACACTAAA
GACCCAACATTGCAAGACAAATTATCAAATTGTTGGAATTCTGCTCCCTTAATGGATGTGGTACAATCAGA
AAGGTAGAAGATCAGTCATTACTACACCAATAATCACCTTCTGCTCATCTCAACTCTGAAGTGTGATCACC
CGTCAGAAACAACCTCCAGATTATTGTGAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATAACATA
GAAGATGATGTAATACAAAGTCACGGCAAAATATAACACCCAGCATGGCTCTTTGAATCCAATTCA
TTTAAAAGACTATACTTGAAATCACCATATTATGTTGACCTTCAAGGAAACTCTTTGTTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGTTGCTGTTCTGATACCTGAGGCCCTCTCCACCTCTGACTTTGCATCTCCAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTGAAAGGTGATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTCTGTGATCTGCACTGTAAGGTTGATATGTGAT
AGCAGTGCACCAAGTCTGCTGCAATCAAGGTTGTGCTCCAGAAGCAACAGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCACAGTGGCAATTCAAGGATTTCAGCAT
GAAACACATGCCAGAAACTCCAAACCAAGGCCCTTCAACAGTGTGCATCTGTTCTCATGGTTCTAGCTCTG
AATGTGGTGAATGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGAGACTACAAATACCAGAAGCTG
CAGAACTATTAAACTAACAGGTCAACCCCTAAGTGAAGACATGTTCTCCAGGATGCCAAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCCTGCATGTAAAAAAA

FIGURE 70

MELVRRLMPLTLIISCLAEI TMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFS YVQLDPGSCESENIVFDGTSSNGPLLGQVCSKNDYVPVFESSSSTLT
FQIVTDSARIQRTVFVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPSTNSGLIGQVCRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCS SDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSVPLNGCGTIRKVEDQSITYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIYITEDDVIQSQN ALGKYNTSMALFESNSFEKTI LESPYV DLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCKVYPLFGHYGRFQFNAFKFLRSMSSVYL
QCKVLI CDSSDHQSRCNQGCVRSKRD ISSYKWK TDSIIGPIRLKDRSASGN SGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGGAGCCTGCAGAGAGGACAGCCGGCTGCGCCG
GGACATGCGGCCCCAGGAGCTCCCAGGCTCGCGTCTCCGTTGCTGCTGTTGCTGC
TGCTGCCGCGCCGCGTGCCTGCCACAGCGCCACGCCTCGACCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCGTGGTTGACCAGGCCAAGTCGGCATCTTCATCCACTG
GGGAGTGTTCGCCCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGAAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAATTAAATGCCAACAGTGGCAGATATTTCAGGC
CTCTGGTGCAAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTGTGGGGGT
CAGAATATTGTGGAACCTGGAATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTCATCCGCTTCTGAGGATGAATCCAGTTCAAGCGGAAATTCCAG
TTCTAAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACTATCAGCCTGAGGTTCTGTGG
TCGGATGGTACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTCTGGCCTGGTT
ATATAATGAAAGCCCAGTCGGGGCACAGTAGTCACCAATGATCGTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATCTTGCCA
CATAAAATGGGAAAACCTGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGAAAGCTGG
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTTCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTCTGGCTAAAAGTCATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATCCAAGCCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGCCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAAC
GATTCTTGAGCAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGCTGGCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGTCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAACGGATAAGAAAATTATGGCAGTTCAAGCCCTTCCCTTTCCACTA
AATTTTCTAAATTACCCATGTAACTTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTAGTAG
CAAGGAATTGGTGGTATTATGGACCGAACTGAAAATTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAACCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTCCTAGGCTACAGACATATAAGCATGTTACTG
AAACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAAATAATGGTGCACCTGTATAGGGCACTTACCCAGGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAATACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCAATTATAAAACATAAGTGTACTGTAACTTACAAACGTTAAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPTWESLDARQLPAWFDQAKFGIFIHG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRGFLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNNYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETY
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHQPLNWI
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCCTGGTCCAAGGCTTTGCGTGAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCCTGTGAGCAAAAAGGCGAACCA
AGCTGAATTCACAGAACAGCTAAGGAGGCCTGTAGGCTGCTGGACTAAGTTGGCGGAA
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAAACTTGAGCTATGGCTGGGTGGAGA
TGGATTCTGGTCATCTCTAGGATTAGCCAAACCCCAAGTGTGGAAAAATGGGGTGGGTG
TCCTGATTTGAAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACATCTGAT
ACTTGGACTAACTCGTCATTCCAGAAATTATCACCACCAAAGATCCCATTCAACACTCA
AACTGCAACACAAACAGAACAGAATTATTGTCACTGACAGTACCTACTCGGTGGCATCCC
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTCCACTTCTATTCCACGG
AGAAAAAAATTGATTGTGTACAGAACAGTTATGGAAACTAGCACCATGTCTACAGAAC
TGAACCATTGTTGAAATAAAGCAGCATTCAAGAACATGAAGCTGCTGGGTTGGAGGTG
CCACGGCTCTGCTAGTGCTCTCCTCTTGGTGTGCAGCTGGTCTGGATTTC
TATGTCAAAAGGTATGTGAAGGCCTTCCCTTACAAACAAGAACATCAGCAGAACAG
CGAAACCAAAGTAGTAAAGGAGGAGAACGGCCAATGATAGCAACCTAATGAGGAATCAA
AAACTGATAAAAACCCAGAACAGAGTCCAAGAGTCCAAGCAAAACTACCGTGC
GCTGAAGTTAGATGAGACAGAACATGAGGAGAACACACCTGAGGCTGGTTCTT
TTACCCCTGCCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAACAGAAAGTCC
GGTTCCCTAACTGGAATCAGCTCAGGACTGCCATTGGACTATGGAGTGC
ACCAAAAGAACATGC
CCTTCTCCTTATTGTAACCTGCTGGATCCTATCCTCCTACCTCAAAGCT
CTTCCACGGCC
TTCTAGCCTGGCTATGCTTAATAATATCCC
ACTGGAGAACGGAGTTTGCAAAGTGC
AAACTGCAAACATCTCATCAGTATCCAGTGGTAAAAGGCC
CTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCACTGAGAACAGCAAGGCTTCT
ACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTCTGAAAGAACACGTATCCC
ACCTGACATGTC
CTTGAGGCCGGTA
AGAGCAAAAGAACATGGCAGAAAAGTTAG
GCCCTGAAAGCCATGGAGATTCT
CATAACTTGAG
ACCTAATCTCTGTA
AAAGCTAAAATAAAGAACATAGAACAAAGGCTGAGG
ATACGACAGTACACT
GTCAGCAGGGACTGTA
AAACACAGACAGGGTCAAAGT
GTTTCTCTGAACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACT
TTTCTGGTCTCTACCACTGCTGAT
ATTTCT
AGGAAATATACT
TTTACAAGTA
ACAAAATAAAACT
CTTATAAATTCT
ATTTTATCTGA
GTTACAGAAATGATT
ACTAAGGAAGATT
ACTCAGTA
ATTGTTAAAAGTA
ATAAAATTCA
ACAAACATTGCTGA
ATAGCTACT
ATATGTCA
AGTGCTGTGCA
AGGTATT
ACACTCTGTA
ATT
TGA
ATTT
ATT
CT
C
AA
ATT
GC
CAC
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AA
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CC
CT
TT
CA
ACA
AG
G
ACT
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AG
AG
AT
GC
AG
AA
AT
TT
GT
GA
CA
AA
AA
TT
AA

FIGURE 74

MARCFSLVLLTSIWTTRLLVQ GSLRAEELSIQV SCRIMGITL VS KANQQLNF TEAK EACR
LLGLSLAGKDQVETALKASFETCSY GWVG DGFVVISRISP NPKCGKNGVGVL IW KVPV SRQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYVASPYSTI PAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKA FPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLEAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCTAATTGCTCTCGTATTGGTGCACGACTTACGATGG
CTCGCCCAACCTTACTACCTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGGAGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACAGAACGGACAAGAGGGTCACGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGAAAGGTGGATGTTGGACGCTACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTGGCTCAACCCCCACCACAGTGTCA
TGGGAAAACAAGAAGGATAAAGATCCTACTTGGCAGTGCTCCTCTCGTCAATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTGG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGGATTGTCAG
GCACCCCTACAGGAAGGCCTGCCATGCTGTGGCCAAGCTGGAGCAAGAAAGAGATC
TCATAGGACGGAGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCCCTTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTAAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCCCAAGGACTCTGCTCCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTATCATTGAAGACAATATTGAACAACCCCTATTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAACCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPLCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMFSKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRAKKLSKAGDNIPEEQPVASTPTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCCTGGGACGTTGCCCTG
GGGCCAGCCTGGCCGGTCACCCCTGGCATGAGGAGATGGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCCGCTCCTACGGACTGCCCTCTACAACGGCTTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCACTGGCAAAGACCTCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCCGGGCGTGTGCGTGTCAAATGGTGGAAAGCT
GTCGGAGAACGGGCCAGAGAGAAGGACGTGCTGGTGGCCATCGGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCCGGGTGTGGTCTTCCTTACCAAGTCCCCA
ACGGCGCTACCAGTCAACTTCCACCGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCCGTG
GTGGCCTCCTTGAGCAGCTCTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCCGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGGCAGCCCTGCCGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACGCCGCCTGCACCGCTATGAT
GTATTCTGCTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGGAC
AGCTTTGCCGCTGGAAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTCACCCGATCCTAACTGTGGGCCAGAGCCTGGGCT
CCGAAGCTTGGCTCCCCGACCCGAGAGCCGTTGTACGGTGTACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGCATTCCCTACTGGCTGTATTGAGTGGTT
CGTTTCCCTGTGGGTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGAAAGCAAACAGAACCCATGCCCTCCCTTGCTCCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGGCCATTGCGGTTTGCGGCTTCTG
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGGCCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCC
CAGCCTGGGGAAGAAGAGGGCCTGGGGGCCCTCCGGAGCTGGCTTGGCCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCAGAACATGAGGAAGGAAGAAACTCCCTCCCCGTTCC
TCCCTCTCGGTTCAAAGAATCTGTTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCGCCAA
AA
AA

FIGURE 78

MGLLLVPLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFPYQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEELDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSGPR
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**ATG**ATGTGGCACCACAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGCGCCCCCTGAGCGACGCTCCCCATGATGACGCCACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGAAAGTGGCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGGGGGAC
GGCGACGGCTGGGTGCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGCAGCGGCA
CATACGGGACTCGGTGAGCGCGGCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCGCCCGTGAAGAAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTCGGACGAGCGCGTTCCGGTGGC
CGACCAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTCCTGCACCCGAGG
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGGTGCAGACGGAGAGGCAGCAGTTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGGTGCTGCCCTGCCAGGACCAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGGAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACCAACGATGAGCT**GTG**AGCACCACGCGACCTGCCACAGCCTCAGAGGCCG
CACAATGACCGGAGGAGGGCCGCTGTGGTCTGCCCTCCCTGTCCAGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTCTGCCCTGGCTCTCAGGGACCCCTGGGTGGCTTC
TGTCCCTGTCACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT
GGCCCCAGCCCTCTCCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGGCCGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSDAGPHQGRVHQAAPLSDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKDGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKGHDGSEVGHVLPPAQDQPLVEANHLLHESDTDKGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTTCCGCACTCGGGCGCAGCCGGGTGGATCTCGAGCAGGTGCGGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGAGGGATCCCTGACGCCTCTGTCCCTGTTCTTGTGCTCCCAG
CCTGTCTGTCGTCTGTTGGCGCCCCCGCCTCCCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCCGAGGGCGCTCCCAGACCTAGAGGGCGCTGGCTGGAGCAG
CGGGTCGTCTGTCTCTCTCGCGCCGCCGGGATCCGAAGGGTGCAGGGCTCT
GAGGAGGTGACGCGGGGCTCCCGCACCCCTGGCCTGCCCCTGCATTCTCCCTCTCCCAG
GTGTGAGCAGCCTATCAGTCACC**ATGTCCGCA**GCCTGGATCCGGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCTGCCGGGCCGCGGGCAGCGAGGGAGGCCGCTCCCATTGCTATCACATG
TTTACCAAGAGGCTGGACATCAGGAAAGAGAAAGCAGATGTCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACACCCGAGAAGAAAAC
CAATAAAGATTGTAAAGCAGACATTGCATTTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGGAAAGTGGCTCTAATGTTGGAAATTGGAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTACTTGAA
AAACTTACATCAGCAAAGATGTTGTTGCCATAAAGGAAGTAGGTTTAGAGGGTA
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCACGGTAGATGCTGGA
GTAAGAAAAGGGATCCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCCAGAGAGTTGGTGTCAATGTATTATAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGCTGT
CGGAATAATGGCTTCTCTTACACATGCCAAGTGGTTGGCACCAAAATACGTAAA
GCCTCTGGTACAGAAGCTGTGCACTCATGAACAAATGATGTGCAAGACCTGTTATAACT
CAGTGAACATTGCCTTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCAAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGCTCTAGCTGTCACTGAGAACATCCGCTATATGAGTGGTGGAACAGCTACTGGT
GATGCCATTCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGCCCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGGCAGTCCTATGATGATGTCCAAGGCCCTGCAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGGTGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTTCTAAACCGAAGGAGTCTCACGCTTCTTACAAGAGAGTTCACAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTAGAGATTCTTACAATCCAGCA**AT**
AATGGTAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGTAATTGTATT
CTCATAATACTGAAATGCTTAGCATACTAGAATCAGATAACAAACTATTAAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTTACAAGGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAAAGAATCTGATACTTAGACCAAAAAAAA

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPLLEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRVYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCCKADIAFLIDGSFNIQRRFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLKNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRLMLEFVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCCGGGCCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCGGCGGGAGCGAGCAGATCCAGTCCGGGCCCGCAGCGCAACTCGGCCAGTCG
GGGCGCGGCTGCGGGCGCAGAGCGGAGATGAGCAGCGGCTGGGCCACCCCTGCTGTGCCTGC
TGCTGGCGGCGGCGGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGTACCCGCAGGAGGAGGCCACCCCTCAATGAGATGTTCCCGCA
GGTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGGTGGAAGAGATGGAGG
CAGAAGAAGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACACTACCTCCAGCTAT
CACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCCACGAGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAATGCCAGTTGCCAGCTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCAGCTGTGTCTGGGTCACTGCACCAAAA
TGGCCACCAGGGGAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCGGCTTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTGTGCCAGTGGCCTCCTCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCACCTCGTGGGGAGCCGTGACCAAGATGGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTTCATGGAGGAGGTGCCAGGAGCTGG
AGGACCTGGAGAGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCAGGCCGCT
GCACTGCTGGAGGGAGAGATTTAGATCTGGACCAGGCTGTGGTAGATGTGCAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTTACA
TCTTCTTCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTTCA
TCCCCCAGGCTGTCTCCAGGCTTCACAGTCTGGTGTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACCAAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTCTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGCAGATGAAATGTTCTGTTCACCCCTGCATTACATGTGTTATTCA
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCAATTGTTCTCCTCGCCATCAGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTTGCCTAACAGTCACACAGCTAGTGAAGACCAGAGCAGTT
CTGGTTGTGACTCTAACAGCTCAGTGTCTCTCCACTACCCACACCAGCCTTGGGCCACCAA
AAAGTGTCCCCAAAAGGAAGGAGAATGGGATTTTCTTGAGGCATGCACATCTGGAATTAA
GTCAAACATAATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCGTCCCTCTAATGAAGACAATGATATTGACACTGTCCCTCTTGGCAGT
TGCATTAGTAACTTGAAAGGTATATGACTGAGCGTAGCATAACAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAAATGAAATTGCAAACATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACACTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGATTCAGAGTTCTTAAAGTTAAAGTTGACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTTGCATTAGAAATCAAGC
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLNLPPSYHNETNTDKVGNNTIHVHREIHKITNNQTG
QMVFSETVITSVGDEEGRRSHECIIDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASGLLCQPHSHSLVYVCKPTFVGSRDQDGIELLPREVPDEYEV
GSFMEEVQRQLEDLERSLTEEMALGEPAAAAALLGEEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTCTGGGCTCAGAAGGACTCTG
AAGATAACAATAATTCAAGCCCATCCACTCTCCCTCCCTCCAAACACACATGTGCATGTACACACACACATACA
CACACATACACCTTCCTCTCCCTCACTGAAGACTCACAGTCACTCACTCTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTTAAGGACAGGGCTGGCCATTACCTCTGCAGCTCTGGCTTGTGAGTCAGTCAAAAAACATGGGAGGG
CCAGGCACGGTGACTCACACCTGTAATCCCAGCATTTGGGAGACCGAGGTGAGCAGATCACTGAGGTCAAGGAG
TTCGAGACCAGGCTGGCCAACATGGAGAAACCCCCATCTCACTAAACATGGGAGAATTCAGGAGGTGAGCAGTCA
AGGTGCTGTAATCCCAGCTACTCAGGTGGCTGAGCAGGAGAATCGCTTGAATCCAGGAGGGAGGATGCAGT
CAGCTGAGTGACCGCTGCACTCCAGCCTGGTACAGAATGAGACTCTGTCTCAAACAAACACGGGAGGA
GGGTAGATACTGCTTCTGCAACCTCTTAACCTGCACTCTTCTTCCAGGGCTGCCCCCTGATGGGCCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GTGAGAATGACTGCCCTGGGAGGGTGGTCTTGGGCCCTGGCAGGGTTGCTGACCCCTAACCTGCAAAACACA
AAGAGCAGGACTCCAGACTCTCTTGTGAATGGTCCCCCTGCACTGTGCCCTGAGCTCACCATGAGGCTTCT
ACTCTTGTAGCTTGGGGCTGGTGCCTGCACTGTGCCCTGAGCTGGTACCCCTGGCATGTTCCCTGCCCCCTCA
GTGTGCTGCCAGATCCGGCCCTGGTATACGCCCGCTGTCCTACCGCGAGGCTACCAACTGTGGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCACACAGACCCCTGCTCTGCAGAGCAACAGCATTGT
CCGTGTGGACCAGAGTGAGCTGGCTACCTGGCCAATCTCACAGAGCTGGACCTGTCCCAGAACAGCTTTGGA
TGCCGAGACTGTGATTTCATGCCCTGCCAGCTGCTGAGCCTGACACCTAGAGGAGAACCGAGCTGACCGGCT
GGAGGACACAGCTTGCAGGGCTGGCAGGCTACAGGAACCTATCTCAACCACAACCAGCTCACCGCATCG
CCCCAGGGCTTTCTGGCTCAGCAACTTGCTGCGGCTGCACCTCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTTGAATGCTGCCAACTTGGAGATACTCATGATTGGGGCAACAGGTAGATGCCATCCTGGACAT
GAACCTCCGGCCCTGGCCAACCTGCGTAGCCTGGTCTAGCAGGATGAACCTGCGGGAGATCTCGACTATGC
CTGGAGGGGCTGCAAAGCCTGGAGAGCCTCTTCTATGACAACCAGCTGCCCGGGTGCCCAGGCGGGCACT
GGAACAGGTGCCGGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAGGGGTAGGGCCGGGGACTTGC
CAACATGTCACCTTAAGGAGCTGGGACTGAAACAACATGGAGGAGCTGGTCTCCATGACAAGTTGCCCTGGT
GAACCTCCGGAGCTGACCAAGCTGGACATCACAATAACCCACGGCTGTCCTCATCCACCCCCCGCCTTCCA
CCACCTGCCCAACATGGGAGACCCCTCATGCTCAACAACACGCTCTCAGTGCCTTGACCCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGGTAGGTTCTCACGGCAACCCATCCGCTGTGACTGTCTCCGCTGGGCAATGC
CACGGGCACCCGTGTCGCTTCATCGAGCCGAATCCACCCCTGTGCGGAGGCTCCGGACCTCCAGCGCTTCCC
GGTCCGTGAGGTGCCCTTCCGGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACAGAACGCTTCCCCAAG
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCGAACCCGAACCCGAGATCTACTG
GGTCACTCCAGCTGGCTCGACTGACACCTGCCCATGCAAGGAGGTACGGGGTGTACCCCGAGGGACCC
GGAGCTGCGGAGGGTGCACAGCAGAACAGGGCAGGGCTATAACACTGTGTGGGCCAGAACCTGGTGGGGCTGACAC
TAAGACGGTTAGTGTGGTTGTGGGCGTGCTCTCCTCCAGCCAGGAGGGACAGAACGGACAGGGGCTGGAGCTCG
GGTGCAGGAGACCCACCCCTATCACATCCTGCTATCTGGGTACCCCAACACAGTGTCCACCAACCTCAC
CTGGTCCAGTGCCTCCCTCCGGGCCAGGGGCCACAGCTCTGGCCGCTGCCTCGGGAAACCCACAGCTA
CAACATTACCCGCTCCTCAGGCCACGGAGTACTGGGCTGCCAGAGCCTTAGGGATCGTCTGGCTCAT
TGCCATCCTGGCTCGCTGTGCTTCTCCTGGCAGCTGGCTAGGGCCACCTGGCACAGGCCAACCCAGGAA
GGGTGTGGTGGGAGGCGGCCCTCCCTCCAGCCTGGCTTCTGGGCTGGAGTGCCTGGGGCTTCTGTCCGGTTGT
GTCTGCTCCCCCTCGTCTGCCCTGGAATCCAGGGAGGAAGCTGCCAGATCCTCAGAAGGGAGACACTGTTGCC
ACCATTGTCTAAAATTCTTGAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTTACAAA
AGAGAACAGCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCTGGCAGCTGGC
CAAGACAGATGGGCTTGTGGGCCCTGGGCTTGTGCTCTGCAAGGACACAGGAGGGACTTGGCTAGGCCCTGC
CCTCTGCTGCCATTCTGAGGAACATCTCCAAGGAACAGGAGGGACTTGGCTAGGCCCTGCCTCCCCATCTT
CTCTCTGCCAGGGCTCCTGGGCCCTGGCTGTGCCCTACCTGTGTGCCCTGGCAAGGGCTGAAGGGGCCACTCC
TCTTCTCTGTACAGTCTCAGTTGCTTGCTCTGTGCTCTGGCAAGGACATTGGAGAGGGATGCCAGGAA
CTCGGGGGCTGCCCTCAATGTGGAGTGAACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCCAGGAA
CGCCTCATCTCAGCAGCTGGCTGGCATTCCGAAGCTGACTTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACCTCCCCAACCGATTCACTCTTCTCTGTAAAAAATAAAAATAACAATAAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFITA
VPPALPAGTQTLQQNSNSIVRVDQSELGYLANLTELDSLQNSFSDARCDFHALPQQLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLNSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDNNFRPLANLRSILVLAGMNLREISDYALEGLQSLSESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPQDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMETMLLNNNALSALHQQTVESLPNLQEVGLHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTDHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADETKTVSVVGRALLQPGGRDEGQGLELRVQETHPYHILLSWTPNNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGRRPLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPSSGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GAAGGCCAAGGCCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGGAGGGGACATTGTGTACCGCC
CTACATGGGCAGACCATCATCAAGGTGATCAAGTTCATCCTCATCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTCGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGTGCCCAACCC
CCTGGCCACACTCTCAAGATCCTGGCGCTTCTACATCAGCCTAGTCATCTTCTACGGCCTCATCTGCATGTA
CACACTGTGGTGGATGCTACGGCGTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCCGCTACTCCAA
GCGCTTCGCCGTCTCTGTGGAGGTGAGTGAGAACAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGGCTACCAAGAACGCGCAGGACAAGCTGGAGCTGCACCTGTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGGAGCTGGAGGTCTCAAGCTGGAGCTGATCCCCGACGTGACCATCCCGCC
CAGCATTGCCAGCTCACGGCCTCAAGGAGCTGTGGCTCTACACACAGCGGCAAGATTGAAGCGCTGCGCT
GGCCTTCTGCGCGAGAACCTGCGGGCGCTGCACATCAAGTCACCAGACATCAAGGAGATCCGCTGTGGATCTA
TAGCCTGAAGACACTGGAGGGAGCTGCACCTGACGGCAACTGAGCGGGAGAACAAACGCTACATCGTCATCGA
CGGGCTCGGGAGCTCAAACGCTCAAGGTGCTGCGGCTCAAGAGCAACCTAAGCAAGCTGCCACAGTGGTAC
AGATGTGGGCGTGCACCTGCAAGAGCTGTCCATCAACAAATGAGGGCACCAAGCTCATGTCCTCAACAGCCTAA
GAAGATGGCAACCTGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGCATCCCCACTCCATCTCAGCCT
CCACAACCTGCGAGGAGATTGACCTCAAGGACAACAAACCTCAAGACCATCGAGGGAGATCATCAGCTTCAGCACCT
GCACCCGCTCACCTGCTTAAGCTGTGGTACAAACACATGCCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGCGCCTCTACCTGAACCGCAACAAGATCGAGAAGATCCCCACCCAGCTTCTACTGCGCGAAGCTGCG
CTACCTGGACCTCAGCCACAACCTGACCTTCTCCCTGCCGACATCGGCTCTCTGCGAGAACCTCCAGAACCT
AGCCATCAGGCCAACCGGATCGAGACGCTCCCTCCGGAGCTTCCAGTGGCAAGCTGCCGCTGGGCCCCGACCT
GGGCAACAAACGTGCTGAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGCAAGTCAGCAGCTGCCGGG
CAACCGCTGGAGTGCCTGCTGTGGAGCTGGCGAGTGCCTACTGCTCAAGCGCAGCGCTGGTGGAGGAG
GGACCTGTTCAACACACTGCCACCCGAGGTGAAGGAGCGGCTGTGGAGGGCTGACAAGGAGCAGGCTTAGGAG
GCCGGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCAGGCCCGAGGGCAGGCTAGCTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGGGCTGGGAGGCTGGGAGGAGCTGGGAGGAGCTGGTGGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCTTCTCCCTGAGACTCACGTCCTCCAGGGCAAGTGTGTTGGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTGGATAATCAGGGTCTCTCCCTGGAGGCCAGCTGCCCCAGGGCTGAG
CTGCCACCAGAGGTCTGGGACCTCACTTTAGTTCTGGTATTATTCTCCATCTCCACCTCCTCATCC
AGATAACTTATACATTCCAAGAAAGTTCAGCCAGATGGAAGGTGTTAGGGAAAGGTGGCTGCCCTTCCCC
TTGTCTTATTAGCGATGCCCGGGCATTAAACACCCACCTGGACTTCAGCAGAGTGGCTGGGGCAACCAG
CCATGGGACGGTCACCCAGCAGTGCCTGGCTCTGCGGTGCGGCCACGGGAGAGCAGGCCCTCAGCTGGA
AAGGCCAGGCTGGAGCTTGCCTCTCAGTTTGTGGCAGTTAGTTTTTTTTTTTTTTTTAAATCAA
AAACAATTTTTAAAAAAAGCTTGAAATGGATGGTTGGTATTAAAAAGAAAAAAACTAAAAAA
AAAAGACACTAACGGCCAGTGGAGCTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGCGCAGGGTGCAGGCTGTCTTCCGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTTTGTGTTTTGGGTTTTGGTGTCTGTTCTTCTCCTCC
ATGTGTCTGGCAGGCACTCATTCTGTGGCTGCCAGAGGAATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTGTGGCTAATCCCCGATGAAAGGTGCTCATTGCCACCTCCCTCTGCTGCCCTGCCCTCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTTCGCCAGACTTGTCTCCACCTCTGCGGCCAG
CCAGTGCCACCGCTGGCTCCGCTGCTTCCATCAGCCCTGCGCACCTGGTCTTCATGAAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCCCTGGGAGGGCAGGGCAGGGCTGGTCTCAAGGCCGTTCCGCTGCC
CTGGAGTGCACACAGCCAGTGGCACCTGGTGGCTGGAAAGCCAACCTGCTTGTAGATCACTCGGTC
AGAAGGGTCCCCGCCCTAGATCAATCACGTGGACACTAAGGCACGTTAGAGTCTCTGTCTTAATGATTATGT
CCATCCGCTGTGCGTCCATTGTGTTCTGCGTGTGTCATTGGATATAATCCTCAGAAATAATGCACACTAG
CCTCTGACAACCATGAAGAAAATCCGTTACATGTGGGCTGAACTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDI PDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQNLNNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFVFLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSKLPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTTGCTGCTGCCGCTGCTGCTGGGCCTGAACGCAGGAGCTGTCAATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCATACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTGAAACTTGAGGAAATTGGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCCGTGGGCACTGGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGGGGGGT
TGCCTGGGTGATTCCCTGGATCTCCCTGTTGATTGGTGCCTCCTGGGGACCTTACCTGT
ACAGCATGTCCTTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGGGTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAAACATCTTAACACTAAAGCACTCCCA
CGTCTACAATGGAGTCAGTCAGATTACACAGAGGCCACCTAGTTGTCTTGTCAAGGC
CACGTGAGACACCTACAACGAGATGCCCTAACAGGCCACCTAGTCATGAATGGCCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATTCTGGGGAGGCCAGGCTACCAACGTCTTGTGAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATAACCATGGGTAGGAGGCCTG
GGTGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCCCTGT
ACAGTGACCCCTAAATCTTGGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTTTC
TACTGGATTCTGAAAGCTGGTCAATGGTTCTCTGACCAAGGGGACATGGCTCTGAAGAT
GATGAGACTGGTGAECTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGCCT
TGGGGCACAGAGCTGAGCTGAGGCCCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCTCT
GGAGGCAATTGGAAATTATTCTGCTTCTTAAAAACCTAAGATTGTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GТИKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGCTGCTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTCGCCATCGTGGGTGGAGAGGACGCCGACTCGGGCGTTGGCCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTTCGTATCGAATATCTATCTGAGCCCTCGTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCTGCACCTGTCACCTACACTAAACACATCCAGCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCACTGCCATCTCCCCACACCCCTCCAGGAAGTTCAGGTGCCATCATAAACA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAAGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCCTT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCCGGTGTCTACACCAATATCAGCCACCACCTTGAGTGGATCCAGAAG
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTCAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAELGRWPWQSLRLW
DSHVCGVSLLSHRWALTAACFETYSDSLDPGWMQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWGYIKEDEALP
SPHTLQEVAIIINNSMCNHLFLKYSFRKDIIFGDMVCAGNAQGGKDACFGDSGGPLACNKNG
LWYQIGVVSWGVGCGRPNPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCACCGCGTCCGGACCGTGGGAAGGGCAGAATGGGACTCCAAGCCTGCCTCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCGGAGCCGACCAGCGAGGACGC
TGCCCCCAGGCTGGGTGCCCCGGACCTGGAGCTGGCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAATGTGAAAGACTCTGGAGCTGGCTGAGGCTGTGAGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCCTAGAGAATGTGGCTGAGCTGGTGGCCATCCC
CACTGACCCCTCCACACGGTCAAAAATGGCTCTGGCAGCCGGAGCCAGAAGTGCCATTCT
GTGATCACACAGGACTTCTGACTTGCTGGCTGAGCATCCGACAAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGGAGGACCTACGGAAACCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTTCCACAGGCCTGGCCCCCATGTGGACTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCCTGTGATCCGTAAGCGATACAACCTGACCTCACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCCTGGAGCAGTATTCCATGAC
TCAGACCTGGCTCAGTCATGCGCCTTCCGGCAACTTGACATCAGGCATCAGTAGC
CCGTGTGGTTGGACAACAGGGCCGGGGCCGGGATTGAGGCCAGTCTAGATGTGAGT
ACCTGATGAGTGCTGGTGCACATCTCACCTGGGCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTTCCTGCAGTGGCTCATGCTGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCCCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCCTGGGTCTCACCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGGTCTGCTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCTCCAG
CCCCTATGTCACCACAGTGGGAGGCACATCCTCCAGGAACCTTCCTCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCACGGCCTTCATACCAGGAG
GAAGCTGTAACGAAGTTCTGAGCTAGCCCCCACCTGCCACCATCCAGTTACTTCAATGC
CAGTGGCGTGCCTACCCAGATGTGGCTGCACCTTGATGGCTACTGGGTGGTCAGCAACA
GAGTGCCATTCCATGGGTGCGAACCTCGCCTCTACTCCAGTGGTTGGGGGATCCTA
TCCTTGATCAATGAGCACAGGATCCTAGTGGCCGCCCCCTTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGCAGGTCTTGTGTAACCCGTGGCTGCCATGAGTCCTGTC
TGGATGAAGAGGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGCTGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGTTGCTGAAGACTCTACTCAACCCCTGACCCTTCATTC
AGGAGAGATGGCTTGTCCCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCCCTGAAA
TGCTGTGAGCTTGACTTCACTCCAAACCTACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCTCAATAAGATGCTGTAACTAGCATTGATGAATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTCCAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCAATTCCCAATTCACTGCAAGGAGACCTCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAATGGCCTCAGTGCATACTCTCAATTTGCTTTATG
GCCTTCCATCATAGTTGCCACTCCCTCTCCTTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCCCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTCATTG
TCCATTGTAGATTGCTCTCAGTTACTCATTGCCCCCTGGAACAAATCACTGACA
TCTACAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATAACCTCAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRTLPPGVSLGRADPEEELSITFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTL ENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLLPGAEFH YVGGPTETHVVRSPHPYQLPQALAPHVDFVGGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLM SAGANISTWVYSSPGRHEGQEPFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLF DVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GGCGCGCGCTCTCCCGCGCCCACACCTGTCTGAGCGGCGAGCGAGCCGGCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTCCTCTC
TTCTTCTGCTCTGTGCTGGCAAGTGAGCCCTACAGTGCCCCCTGGAAACCCACTTG
GCCTGCATACCGCCTCCCTGCGTCTGCCCCAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAACCT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGGCCAAAC
ACCGAGACTCAGGGCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGTGGCAGAGAACATGTCTCACAGCTGCCACTGCA
TACACGATGGAAAAACCTATGTGAAAGGAACCCAGAACGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGGCCAACGACTCCACTTCAGCCATGCCGAGCAGATGAA
ATTCAGTGGATCCGGGTGAAACGCACCCATGTGCCAAGGGTTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCCTGGAACTCAAAAGCCCCACAAGAGAAAA
TTTATGAAGATTGGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGCCAGCGGGTCTGGGTCTAT
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTTACCAAGCAATGCGATGCCAGCCAGGGGCCAGCGGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACAGTGGGAGCAGGAAATTATTGGCATTTCAGG
GCACCAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGG
TGACACAGTGGCTCGCAGCAATTAGGGCTTCATGTTCTTATTTAGGAGAGGCC
AAATTGTTTTGTCATTGGCGTCACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAATG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGCAATGAGGAATATTGACAATTAGTTAATCTCACGTTTG
CAAACTTGATTTATTCATCTGAACTTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAA

FIGURE 96

MAGIPGLLFLLFFLLCAVGQVSPYSAPWKPTWPAYRLPVVLPQSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTETQVG
IYIILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTS
VKLSTGCTGTLVAEKHV
LTAACIHDGKTYVK
TQKLRVGFLKPKFDGGRGANDSTS
SAMPEQMKFQWIRVKRTHVPKG
WIKGNANDIGMDYD
YALLELKKPHKRKFMKIGV
SPPAKQLPGGRIHFSGYDNDRPGNLVYRFCDV
KDETYD
LQQCDAQPGASGSGVYV
RMWKRQQQKWERKIIGIFSGH
QWVDMNGSPQDFNV
AVRITPLK
YAQIC
YWIKG
NYLDCREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCGCCCCAGCCCTGGGTGGGGCTGTCTGGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATACTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACC GGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCAC TGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCCACTGTTCAAGGACAACCTGAACAAACCATACTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTGGTCCCAGAAGGTGGGTGTTGCCTGGGTGGAGC
CCCACCTGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCTCAGACCCTGCAGAACGCTGAAGGTTCTATCATCGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTTGCGCACCGCTCTGGTGGAGAACGATCGTCAAGGGTGCA
GCTCCGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCCG
CCGGCGCTCCTAGGGCGCAGCGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGCGGCGGCCTCGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGCCGGACGGCTGCTGCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCCGGGCCAGCGCTTTGTATATAATGTTAATGATTTTAT
AGGTATTTGTAACCCTGCCCACATATCTTATTATTCCCTCCAATTCAATAATTATTATT
CTCCAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAAHCFKDNLNKPYLF SVLLGAWQLGNPGSRSQKVGVVA
WVEPHPVYSWKEGACADIALVRLERSIQFSERVLPICLPDASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC SHLYWRGAGQGPITEDMLCAGYLEGERDACLGDGGPLMC
QVDGAWLLAGIISWGEGCAERNRPGVYISLSAHRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGGCCCGTTGGAGCCCTCACAGATGAGGAGAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCAGTGGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGCGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCACCTCTGTGAGAAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCACTGCAAGAACTCCCTCTGTGAACCCATCGGAAGC
CCGGAAGATGCTCAGGATTGCCTTACCTGGTAAC TGAGGCCCATCCTCCGGCGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC
AACTGAGGTCCCTTCCATTGGCAGCTCACAGCCTGCCCTCCTGGATGAGGAGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCTCTAGGAGGCCAGAGAACTCTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACTCCTACCCCATGCCAGGAGGAGGCTGAGGCTGAGGCTGAGTTGCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGCATGTGTGGGCCCTCCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTGAATGGGATACCAACTCAAAGGG
TGAAGAGGTCA GCTGTCCCTGTCA TCTTCCCCACCCCTGTCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGAAGGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGGAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGGATGGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTC
TTTGAGTGGGGAGGCAGGGACGGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKR LMVELHNLYRAQVSP TASDMI HMRWDEE
LAAFAKAYARQCVWGHNKERRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQ
MCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGTPCSQC
PSGYHCKNSLCEPIGSPEADAQDLPYLVTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEV
SGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSI LAAHSLPSLDEEPVTFPKS
THVPIPKSADKVTDKVPSRSPENS LDPKMSLTGARELLPHAQEEAEAEALPPSSEVLAS
VFP AQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAE GPDKPSVV
SGLNSGPGHVWGPLLGLLLPPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237,
250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAAAGTCAGGCTTTCAATTGGGAAGCCCCCTCAACAGAACCGGTCAATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCTGCTTACATTAGCAGACCGGACTTAAGTCACAACAGATTATCTTCAT
CAAGGCAAGTCCATGAGCCACCTCAAGCCTCGAGAAAGTGAACACTGAACAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTCCCTGAAACTTGGACCTAGCAGAACAAATATTCAAGAGCTCCAAACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGAACCGAGTCACATCAATGAAACCTGGGTATTTGACAA
TTTGGCCAACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCCAAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTTAAAGTAGATGGACTGACATTCCAAGGCCTGG
TGCTCTGAAAGTCTGAAATGCAAAGAAATGGAGTAAAGAACCTATGGATGGAGCTTTGGGGCTGAGCAA
CATGAAATTTGCACTGGACCATAACAAACCTAACAGAGATTACCAAGGCTGGTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAACGCTCAG
TGAGCTGGACCTAACTTCAACTTCAAGGTTAGATGATTCAAGCTTCTGGCTTAAGCTTAAACTAAATAC
ACTGCACATGGAACAAACAGACTCAGCTACATTGCTGATTGCTCTCCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAGAACATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGCTTGACAAACACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCA
TCTAGACCTGAGTGAACACGCAATCATGTCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAACTT
GCATTAAATACATCAAGCTTTGTGCAATTGCAAGCTAAATGGCTCCACAGTGGGTGGCGAGGTGATGGAGTATACAC
TCAGAGCTTGAAATGCCAGTTGTGCCCCATCCTCAGCTGCTAAAGGAAGAACGATTGGCTGTTAGCCAGA
TGGCTTGTGTTGATGATTTCACAAACCCAGATCACGGTCAAGCCAGAACACAGTCGGCAATAAAAGGTT
CAATTGAGTTCATCTGCTCAGCTGCCAGCAGTGAATTCCCAATGACTTTGCTTGGAAAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGGAAATTATGCAACACCTCCGGGCCAACGGTGGCAGGGATGACGTGTTTATCGT
CATCCCTCGGCTGCGCAGGTGGAATTGCACTGAGGGAAATATCAGTGTGTCATCTCAATCACCTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCATGGATCTCACCAT
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAACGGA
TGGGGGACAGACTTCCAGCTGCACGGAGAGACGCATGCATGTGATGCCAGGGATGACGTGTTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTCAAGAACGGAGAACAGC
AACTCTGACTGCTCTAGAAACACCATCATTGGCCACTGTTGGACCGAATGTAACCAAGGGAGAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACCTGGACCAAAGATGATAGCCCATTGGTGG
AACCGAGAGGCACTTTTGCAAGCAGGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGTGATGGGAA
ATACACATGTGAGATGCTAACACCCCTGGCACTGAGAGAGGAAACGTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCACTCGTAGACGATGACGGATGGCCACTGTGGGTGTCATAGC
CGTGGTTGCTGTGGGGCACGTCACTCGTGGGTGTCATCATACACACAAAGGCGGAGGAATGAAGA
TTGCACTAACACACAGATGAGACCAACTTGCAGCAGATATTCTCTAGTTGTGATCTCAGGGAACGTT
AGCTGACAGGCAAGGATGGGTACGTGCTTCAAGAAAGTGAAGCCACCAAGTTGTCACATCTCAGGTGCTGG
ATTTTTCTTACACACATGACAGTAGTGGACCTGCCATTGACAATAGCAGTGAAGCTGATGTGGAAGCTGG
CACAGATCTGTTCTTGCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGAAATGTGATGGCTCAGA
TCCTTTGAAACATATCATACAGGTTGCACTGCCAACAGTTAAATGGACCAACTATGAGCCCAGTTA
CATAAAGAAAAGGAGTGCCTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATATC
GTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTAAAGTTAGTTAGTGCACAGGCCAGCGTCGGTGCCTCGAGTAATTCTTCTATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCTTCAAGCTTGGACAGCCATCAGATTGTGAGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCCAGACTTGGACTCTGGGTAGAGGAAGATGGGAAAGAACAGAC
AGATTTCAAGGAAGAAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAAATTTCA
TTATGACTGGACACATGACTGAATGAGACCAAAGGAAAAGCTTAAACATACTACCTCAAGTGAACCTTATT
AAAGAGAGAGATCTTATGTTAAATGGAGTTATGAATTAAAGGATAAAATGCTTATTATACAGAT
GAACCAAATACAAAAAGTTATGAAAATTAAACTGGGAATGATGCTCATATAAGAATAACCTTTAAACTA
TTTTTAAACTTGTGTTATGCAAAAAAGTATCTACGAAATTAAATGATATAATCATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT
TTAAATAGAAGTTACTTCATTATATTGCACTTAAATAAAATGTGCAATTGAA

FIGURE 102

MVDVLLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE
FCQKLSLELDLTFNHLRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSITKKAFTGDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQCLKWLPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTVNMLPSFTKTPMDLTIRAGA
MARLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQN
SAGSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPQLNWTKDDSLPLVTER
HFFAAGNQLIIVDSDVSAGKYTCMSNTLGERGNVRLSVIPTPTCDSPQMTAPSLLDDG
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADI PSYLSQGTLAD
RQDGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCSPDPRTVLMDHYEPSYIKKKECYPCHPSEESCERSFSNISW
PSHVRKLLNTSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLNYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCTCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTGTGAGCCCTGGATCTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTAGACCCGCGGGGTTGGTGTGTTCTGACATAAATAATCTAAAGCAGCTTCCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTACAAAGAAAAAGTATGTTCTTCTC
TATAAGGAGAAAGTGAAGCAAGGAGATATTTGGAATGAAAGTTGGGCTTTTAGTAAAGTAAAGAAGT
GGTGTGGTGGTGTTCCTTCTTTGAAATTCCCACAAAGAGGAGAGGAAATTAATAACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGGGCAGATTGAGGATTGAGGATTTCTCATCAACCTCTTCTTAAAT
TTTGTGCTATGTTGACTAAAATGACGGATAATTGCAAGGTTCTTCAACCCACCTGGATTTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACCTGTTGAATTCCAGAACGGACAAACACCAGATAAAATTATGAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTCCTAGGTTAACAGGGCCCTATTGACCCCTGCTTGTGGTGT
GCTGGCTCTCAACTTCTGTGGTGGCTGGCTGGTGGCTCAGACCTGCCCTCTGTGCTCCTGCAGCAA
CCAGTTCAAGGATGATTGTTGCGAAAACCTGCGTGAGGTTCCGGATGGCATCTCCACAAACACAGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGACTTCAAGCAGTTGAGGCACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCATATTGGGCTTCAATGGTCTGGCAACCTCAACACTCTGGA
ACTCTTGACAATCGTCTTACTACCATCCCGAATGGAGCTTTGTATACCTGCTAAACTGAAGGAGCTGTT
GCGAAACAACCCATTGAAAGCATCCCTCTTATGCTTTAACAGAACTCCTCTTGCAGCAGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACCTGAGGTATTGAAACCTTGC
CATGTGCAACCTTCGGAAATCCCTAACCTCACACCGCTCATAAAACATAGATGAGCTGGATCTTCTGGAAATCA
TTTATCTGCCATCAGGCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGATTGAAACGGAATGCCTTGACAACCTTCAGTCACTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTTCACTCCCTGATCATCTAGAGCGATACATTACATCACAAACCTTGGAAACTG
TAACCTGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCCCTGAACACAGCTTGTGCCCCGGT
TAACACTCCTCCAATCTAAAGGGGAGGTACATTGGAGAGCTGACCAGAATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAAGACCTCAATGTCACTGAAGGCATGGCAGCTGAGCTGAAATGTGGCCCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAATGGAACAGCTCATGACACATGGGGCGTACAAAGTGGGATAGCTGT
GCTCAGTGTGGTACGTTAAATTCAAAATGTAACTGTGCAAGATACAGGCATGTACACATGTATGGTGGTAA
TTCCGTTGGAAATACTACTGCTTCAGCCACCTGAATGTTACTGCAAGAACACTACTCTTCTTACTTTTC
AACCGTCACAGTAGAGACTATGGAACCGTCTCAGGTGAGGACGGCACGGACCAGATAACAAATGTGGGCTCCACCTC
AGTGGTCAGTGGAGACCAATGTGACCACCTCTCACACCAAGAGCACAAAGTGGCAGAGAGAAAACCTT
CACCATCCCAGTGAATATAAACAGTGGGATCCCAGGAATTGATGAGGTATGAAGACTACCAAAATCATCAT
TGGGTGTTTGTGGCCATCACACTCATGGCTGCAGTGTGCTGGTCTTCAAGATGAGGAAAGCAGCACCA
TCGGCAAAACCATCACGCCAACAAGGACTGTTGAAATTATTAAATGTGGATGAGATTACGGGAGACACACC
CATGGAAAGCCACCTGCCATGCCCTGCTATGGCATGAGCACCTAAACTACTACATACAAATCTCCCTT
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTCACTGCATGAAACCGTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAAATCTAAACATTACAGGTTACAAAAAAACAAACATCAAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTATTAAAGCAGACAAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIIVKNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRLNNPIESIPSYAFNRIPSLRRLDGELKRLS
YISEGAFEGLSNLRYLNLAMCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLHHNPWCNCIDIL
WLSWWIKDMAPSNTACCACRNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTQDTGMYTCMVSNVGN
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIIINVDEITGDTPMESHLPMPAIEHEHLNHYNSYKSPFNHTTVNTINSIHSS
VHEPLLIRMN SKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

FIGURE 105

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRIASIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLYGLLMLQELHLSQNAINRISPDAWEFC
QKLSELDLTFNHLSRLDDSSFLGLSLLNLTIGNNRVSYIADCAFRLGSSLKTLDLNNEIS
WTIEDMNGAFSGLDKLRRLILOQNRIRSIKKAFGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLHLNTSSLLCDCQLKWLPOWVAENNQSFVNASCAPQQLLKGRSIFAVSPDGFVCDDF
PKPQITVQPETQSAIKGSNLASFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCTAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPVVTERHF
FAAGNQLLIIVDSDVSDAGKYTCMSNLTGTERGNVRLSVIPTPTCDSPQMTAPSLLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADIPSYLSSQGTLADRQ
DGYVSSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLCFLCPFLGSTGPMY
LKGNVYGSDFPETYHTGSPDPRTVLMHDYEPSYIKKKECYPCHSEESCRSFSNISWPS
HVRKLLNTSYSHNEGPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDAYS
SFGQPSDCQPRAFYLAHSSPDLDGSEEDGKERTDFQEENHICTFKQTLHENYRTPNFQSYDLDT

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519, 688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378, 383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735, 799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022, 1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433, 513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAAACTTGCCTCGCGGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCCAGGCCGGAGCGCAGCTGAGAC
TGGGGGAGCGCTTCGGCTGTGGGCGCCGCTGGCGCCGGGGCGCAGCAGGAAGGGAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCGGGAGAGCCTGGTGGTCCCGTCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGAAAGGCAGCGGAGGAGGGCTATGGTGAGCAAGGAGGCCGCTGATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCGAGGAGGCAGAACAGCCTGCC
TCCATCAGCCCTGGCGCCAGGCGCATCTGACTCGGCACCCCTGAGGCACCATGGCCAGAGGCCGGTGTGC
TGCTCCTGCTGCTGCTGCCACAGCTGACCTGGGACCTGTGCTTGCCTGAGGGGCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGAGGCCGTGCTGTACTGAGCCCTGAGG
AGCCCGGGCTGGCCAGCCGGTCACTGCCCCGAGACTGTGCTGTTCCAGGAGGGCGTGGACTGTG
GCGGTATTGACCTGCGTGAGTCCCCGGGACCTGCCTGAGCACACCAACCCTATCTGCAGAACAAACCAGC
TGGAAAGATCTACCCCTGAGGAGCTCTCCGGCTGACCCGGTGGAGACACTGAACCTGAAAACAACCGCCTGA
CTTCCCAGGGCTCCCAGAGAACGGCTTGGAGCATCTGACCAACCTCAATTACCTGTACTGACTTGGCCAATAACAAGC
TGACCTTGGCACCCGCTTCCGCAAAACGCCCTGATCAGTGTGACTTTGCTGCCAACATCTCACCAAGATCT
ATGGGCTCACCTTGGCAGAACGAAAATTGAGGTCTGTGTACCTGCACAACAAACAGCTGGCAGACGCCGGC
TGCCGGACAACATGTCACGGCTCCAGCAACGTGAGGTCTCATCCTGTCAGCAACTTCCGTGCCACGTG
CCAAGCACCTGCCCTGCCCTGTACAAGCTGACCTCAAGAACAAACAGCTGGAGAAGATCCCCGGGGC
TCAGCGAGCTGAGCAGCCTGCGAGCTATACTGAGAACAAACTACCTGACTGACGAGGGCTGGACAACGAGA
CCTTCTGGAAGCTCTCACGCTGGAGTACCTGGATCTGTCAGCAACACCTGTCTGGTCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACCTGGAGAACGACGCAACCGCTGCCAGGGCATCCACCCACTGGCCTCCAGGGC
GCAGCCTGGAGTACCTGCTGCTGCACAGCAACCGAGCTGCCAGGGCATCCACCCACTGGCCTCCAGGGC
TCAAGCGGTTGACACGGTGCACCTGTACAACAAACGCGCTGGAGGCCGTGCCAGTGGCCTGCCCTGCGCGTGC
GCACCCCTCATGATCCTGACAACCAAGATCACAGGCAATTGGCGCGAAGACTTGGCACCACCTACTTCTGGAGG
AGCTCAACCTCAGCTACAACCGCATCACCAGCCCACAGGTGCACCGCAGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTCGGCAACCGCTGCACACGCTGCCACCTGGCTGCCATGGTCAAGGTTAACAAGC
TCAAGCGCAATGAGCTGGCTGCCATTGGCACAGAGGGCGCTGGCGGGCATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCGAGCCTGGGCCCGTGGCCTGGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGGCTCCCCGAGTCAGTACCTGAGTACCTGAGAACAA
AGATTAGTGCCTGGCTGGGCAAGCTGCCCTCGACTCCACGCCAACCTCAAGGGATCTTCTCAGGTTAACAGC
TGGCTGTGGGCTCCGTGGTGGACAGTGCCTCCGGAGGTGAAGCACCTGAGGTCTTGACATTGAAGGCAACT
TAGAGTTGGTACATTCCAAGGACCGTGGCCCTTGGGAAGGAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACGCCGACTTTCTGC
AGCACACGCCCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACAGAACACCCAGTCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCACGGCGTGTGCCACGGCCAGACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACCTACCCCTCAAACACCACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTGTAATCATGCAGGGAAGGGCTGCCCTGGCACACACAGGCACCCA
TTCCCTCCCCCTGCTGACATGTGATGCGTATGCATACACACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAGCCTATGCCACAGACAGCTTGCCTGCCAGGCCAGAATCAGCCATAGCAGCTGCCGTCTGCC
GTCCCATCTGTCCTGCCCTGGAGAACACAGGTATCCATGCTCTGTCAGGCTGCCACGGCTGCCACCCCTCT
GGAACTCACAAAAGCTGGTTTATCCTTCCATCCTATGGGACAGGAGCCCTCAGGACTGCTGGCCTGGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGCAGTCACTCTGCTAAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACCTTCCAATGGCAAGCCAGTGGAGGCAGGATGGAGAGGCCCTGGGTGCTGCTGGGGCTTGGGG
CAGGAGTGAAGCAGAGGTGATGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTCAGGCCTGTGGGGAAAGTCCGGTGCCTTATTCTTATTCTTCTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAAACTAATATAAAAGCATTATCCCTATCCCTGCAAAAAAA

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAAEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVTLMILHNQITGIGREDFATTYF
LEELNLSYNRITSQVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNEALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCGCAGCAGACCTGCTCCGGCCGCGCTGCCGCTGCTCTCCGGGAGCGGCAG
CAGTAGCCCGGGCGGCAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCTCCCATGGCAGCCACCA
CAACCTGTTCTCGCGGCCACTGCGCTGCCAGGACCCGCTGCCAACATGGATTCTCTGGCCTGGT
GCTGGTATCCTCGCTCACCTGCAAGGGCCCGAGTCAGCAGGGAGGTGGCCAGGAAATAGTGTATCGAT
TGGCTATGCTTATGGAGGATTGACTGCTGCTGGGCTGCCAGTCTGGGACAGTGTAGCC
TGTGTGCCAACACGATGCAAACATGGTAATGTATCGGCCAAACAAGTCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGCCCCGCCCTGTAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTGTACTGCTCAACGGATATATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAACTGTCAGTATGGCTGTGATGTTAAGGACAAATACGGGCCAGTGCCATCCCTGGCCT
GCACCTGGCTCTGATGGAGGACCTGCTGTAGATGTTGATGAATGTGCTACAGGAAGGCCCTGCCCTAGATT
TAGGCAATGTGTAACACTTTGGGAGCTACATCTGCAAGTGTGCTAAAGGCTCGATCTCATGTATATTGGAGG
CAAATATCAATGTATGACATAGACGAATGCTCACTTGGCTAGTATCAGTGCAGCAGCTTGCTCGATGTTAA
CGTACGTGGGCTTACAAGTGCACAAATGTAAGGAGGATACCAAGGGTGTGGACTGACTTGTGTATATCCAAA
AGTTATGATTGAAACCTTCAGGTCACATTGTAACAAAGGGAAATGGTACCATTTAAAGGGTGAACACAGGAA
TAATAATTGGATTCTGATGTTGGAAGTACTTGGCTCGAACACCATATATTCCCTATCATTACCAA
CAGGCCTACTCTAAGCAACACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCAACCCAC
CCTGCCAACAGAGCTCAGAACACCTTACCCACCTACACCCAGAAAGGCCAACCAACGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTGAGAAACCCAGG
AGATGTGTCAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTTGGATGGATCAGGGAGAAAGACAA
TGACTTGACTGGAACCAATCAGGGACCCAGCAGGTGACAATATCTGACAGTGTGGCAGCAAAGCCCCAGG
GGGAAAAGCTGCACGCTGGTGTACCTCTGGCCGCTCATGCATTGAGGGACCTGTGCTGTGATTAGGCA
CAAGGTGACGGGCTGCACTCTGGCACACTCCAGGTGTTGTGAGAAAACAGGTGCCACGGAGCAGCCCTGTG
GGGAAGAAATGGTGGCCATGGCTGGAGGAAACACAGATCACCTTGCAGGGCTGACATCAAGAGCGAATCACA
AAGATGATTAAGGGTTGGAAAAAAAGATCTATGTTAAAGGAACAGGACTGGATTATTGAGGCTGGAGAAG
AGAAGACTGAGGGCAAACCAATTGATGGTTTCAAGTATATGAAGGGTTGGCACAGAGAGGGTGGCACCAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GCCATTGTTAGAATACTCATAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTCTTCTAAAAAATTAGA
AAAAAATTGCTATTAAAGATGGTTAAAGATGTTCTACCAAGGAAAGTAACAAATTATAGAATTCCCAA
AGATGTTTGATCCTACTAGTAGTATGCACTGAAATCTTAGAACTAAATAATTGGACAAGGCTTAATTAGG
CATTTCCCTCTGACCTCTAACGGAGAGGGATTGAAAGGGGAAGAGGCCACAAATGCTGAGCTCACTGAAATA
TCTCTCCCTATGGCAATTCTAGCAGTATTAAAGAAAAAGGAAACTATTATCCAAATGAGAGTATGATGGAC
AGATATTGTTAGTATCTCAGTAATGCTCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTTCAATGGATGATGTTCAAGATTGTTCTTAAAGAGATCCTCAAGGAACACAGTTCAGAGAG
ATTTTCATGGGTGCATTCTCTGCTTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGGCCCTGCCCC
ACACCCGGCAGACCTTCCCTCACCTCATCAGTATGATTGATTCTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTCTGTCATTAAACCTGGTAAAGGCAGGGCTGG
AGGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGTAGATCCATTAAATGGTTATT
TCCATTGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTACTTTGATGCCAA
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTTATTATTAAATGTTT
CTAAAATAAAAATGTTAGTGGTTTCAAATGGCTAATAAAAACAATTATTGTAATAAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGE CIGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRQC
VNTFGSYI CKCHKGFDL MYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYI PKVMIEPSGPIHVPKGNGTILKGDTGNNNWI PDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPA AASTPPGGITVDN
RVQTDPQKPRGDVF SVL VHS CNFDHGLCGWI REKDNDLHWEPI RD PAGGQYLT VSAAKAPGG
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSGTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAGACAGGTGCTGCTGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGAATACC
AACACAAGTTCACCATGATGCCACCCAAATGCATCTGCTTATCAACCCACTGCAGTTCCCT
GATGAAGGCAATTACATCGTGAAGGTCAACATTCAAGGAAATGGAACACTATCTGCCAGTCA
GAAGATAACAAGTCACGGTTGATGATCCTGTACAAAGCCAGTGGTGCAAGATTCACTCCCT
CTGGGGCTGTGGAGTATGTGGGAAACATGACCCCTGACATGCCATGTGGAAGGGGCACTCGG
CTAGCTTACCAATGGCTAAAAAAATGGGAGACCTGTCCACACCAGCTCCACCTACTCCTTTC
TCCCCAAAACAATACCCCTCATATTGCTCCAGTAACCAAGGAAGACATTGGGAATTACAGCT
GCCTGGTGAGGAACCCCTGTCAGTGAATGGAAAGTGATATCATTATGCCCATCATATTAT
GGACCTTATGGACTTCAAGTGAATTCTGATAAAGGGCTAAAGTAGGGGAAGTGTACTGT
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGCCTCGCTTAGAAGTT
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTTACAACAAACATAAC
CGGCAGGCAAGATGAAACTCATTCACAGTTATCATCACTCCGTAGGACTGGAGAAGCTG
CACAGAAAGGAAATCATTGTCACCTTAGCAAGTATAACTGGAATATCACTATTGATT
ATATCCATGTGTCTCTCCATGGAAAAAAATCAACCCCTACAAAGTTATAAAACAGAA
ACTAGAAGGCAGGCCAGAAACAGAACAGGAAAGCTCAAACATTTCAGGCCATGAAGATG
CTCTGGATGACTCGGAATATGAATTGTTGCTTCCAGATGTTCTGGTGTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTGTGTATGGGCAAGATTGCACAGTACAGT
GTATGAAGTTATTCAAGCACATCCCTGCCAGCAGCAAGACCATCCAGAGT**GAAC**TTTCA
GCTAACAGTACATTGAGGTGAAGAAATTCTGAAGAAACATTAAAGGAAAAACAGTGGAAAAGT
ATATTAACTGGAATCACTGAAGAAACCAGGACCAACACCTCTACTCATTATTCC
TGCAGAACAGGAAACATGTTGGGAAATTCCCTCAGTGGAGAGTCGTTCTGCTGACGG
GGAGAACGAAAGTGACAGGGGTTCCCTCATAAGTTGTATGAAATATCTCTACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCACCTACAAA
TGTGGAAACTTACATTGTTGCTGATTTCAGCAGACTTGTATTAAATTGTTATTAGTG
TTAAGAATGCTAAATTATGTTCAATTATTCCAAATTCTATCTTGTATTGTACAA
CAAAGTAATAAGGATGGTTGTCAACAAAAACAAACTATGCCCTCTTTTTCAATCACC
AGTAGTATTGGAGAAGACTTGTGAACACTTAAGGAAATGACTATTAAAGTCTTATTGTTA
TTTTTTCAAGGAAAGATGGATTCAAATAATTATTCTGTTTGTCTTAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSPHTVHGVRGQALYLPVHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCTSADSHPPNTYSWIRRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLPLASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSVPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGCTGTT
GCTTGGGGTGCTCCCTGGACGCACGGCGGGAGCAACGTTCGCGTCATCAGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTATGCCCGTGGTGCCTGCT
TGTCAAAATCTCAACCGGAATGGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTTATCATTGTAAGATGGTGAATTAGGCCTATCAGGGTCCAAGGACTAAG
AAGGACTTCATAAAACTTTATAAGTGATAAAGAGTGGAGAGTATTGAGCCGTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTCTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTTATTGAAAGACCTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTCCGGACTGTTATTAGGACTCTGTATGATATTGTGGC
AGATTGCCTTGTCCCTCAAAAAGGCGCAGACCACAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAACTGCACAAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAAGAAGCTGAAAGTAAAGAAGGAACAAACAAAGACTTCCACAGAATGC
CATAAAGACAACGCTCTGGTCCATCATTGCCACAGATAAATCCTAGTTAAATTATAG
TTATCTTAATATTATGATTTGATAAAACAGAAGATTGATCATTGGTTGGTTGAAGTG
AACTGTGACTTTTGAAATATTGCAAGGTTCACTAGATTGTCATTAAATTGAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAAGCACAGTATGATG
GTTAAATAGTTCTTAATTGGAAAAACTCGTGCCAAGCAATAAGATTATGTATATTGT
TTAATAATAACCTATTCAAGTCTGAGTTGAAAATTACATTCCCAAGTATTGCAATTAT
TGAGGTATTTAAGAAGATTATTTAGAGAAAATATTCTCATTTGATATAATTCTCTG
TTCACTGTGAAAAAAAGAAGATATTCCATAAATGGGAAGTTGCCATTGTCTCAAG
AAATGTGATTTCAGTGACAATTCTGGTCTTTAGAGGTATATTCCAAAATTCTTGT
ATTTTAGGTTATGCAACTAATAAAACTACCTTACATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTTAAGTTCATGGTATTCTTGTGATTC
CAACAAAGTTGATTCTGTATTCTTACTTACTATGGTTACATTTTTATT
CAAATTGGATGATAATTCTGGAAACATTTTATGTTTAGAAACAGTATTCTTGT
GTTCAAACGTGAAAGTTACTGAGAGATCCATCAAATTGAACAACTGTTGAATTAAATT
TTGCCACTTTTCAGATTACATCATTCTGCTGAACTTCAACTGAAATTGTTTTT
TTCTTTTGGATGTGAAGGTGAACATTCTGATTGGTCTGATGTGAAAAAGCCTGGTA
TTTTACATTGAAATTCAAAGAAGCTTAATATAAAAGTTGCAATTCTACTCAGGAAAAG
CATCTTCTGTATATGTCTTAAATGTATTGGCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTGATGTTAAAATAACATTATTTTATATTAAAGACAA
ACTTCATATTCTGTGTTCTTCTGACTGGTAATATTGTGTTGGGATTCACAGGTAAA
GTCAGTAGGATGGAACATTTAGTGTATTCTAAAGAGCTAGAATACATAGTTT
CACCTTAAAGAAGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGAC
AATTCTGTAATGTCCCCTTCTTAGGCTCTGTTGCTGTGAATCCATTAGATTACAG
TATCGTAATATACAAGTTCTTAAAGCCCTCCTTAGAATTAAATATTGTACCATT
AAAGAGTTGGATGTGTAATTGTGATGCCTTAGAAAATATCTAACGACAAAATAAACCT
TTCTAACCACTTCATTAAGCTGAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGAPWTHGRRSNVRVITDENWRELLEGDWMIEFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPPSKLLSESAQPLKKVEEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGGACAGGCGGATTGGAAGAGCGGG
AAGGTCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACCTGAAACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGGCAATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGCTACCTGGCTCACCTGTGAATGCCTACAAACTGG
TGAAGCGGCTAACACACAGACTGGCCTGCGCTGGAGGACCTTGTGCTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGAGCAGATAGG
AGCTGCCAACGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACCAAGGCAATGCTGAGTGTGGATGACTGCTTTGGGATG
GGCCGCTCGGCCTACAATGAAAGGGACTATTATCATACTGGTGTGGATGGAGCAGGTGCT
AAAGCAGCTGATGCCGGGGAGGAGGCCACCACAAACGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCCTGCCCCCTGGAGGCTACCCGCCCTGCTC
TCCCTGACCCAAAGCCACGAACGAGCTGGAGGGAATCTGGTACTTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAAACGTTAACAAATCAGACAGAACGACTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCCCTGAGAGGGATGTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAAACACTGACACCCCTAGACAGAACAGAGGCTTTCTGTAGGTACCAACATGGCAA
CAGGGCCCCACAGCTGCTCATGGCCCTTCAAAGAGGAGGACAGTGGACAGCCCGCACA
TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGCAAAA
CCTAAACTGCACGAGCCACCGTTGATCCAAAGACAGGAGCCTCACTGTCGCCAGCTA
CCGGGTTTCAAAGCTCCTGGCTAGAGGAAGATGATGACCTGTTGGCCCGAGTAAATC
GTGGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGGAGGAACAGTATGAACCGCACTCGACTTCTCTAGGCACCTTTGACAGCGG
CCTAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAACAGGTTACAGCTGTG
TTCTGGTACAACCTCTTGCAGGGGAAGGTGACTACCGAACAAAGACATGCTGCCCTG
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAACGAGTTGACTTGACATCCTTTCTGCTCTCCCTG
CTTCAGCCCATGTCACCGTACAGAACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCGGAGCAGAGGGAGACCATACTAGGGCGACTCCTGT
GTGACTGAAGTCCCAGCCCTTCCATTGAGGCTGTGACCGCTAGCAAGGTGCCTTGTACCTCAGGTGTT
AAGTGGCTGAGCAGAGTTAGCTGTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACAAAAAATGTCCTACCAAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSGVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKIKSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDDYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRAELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVYDYLPERDVYESLCRGEVKLTPRRQKRLF
CRYHHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHDFDS
RRPFDGKTEGNRLATFLNYMSDVEAGGATVFPDLGAAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEVD

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCCTTTAGTGGAAAGACAGACCATATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTTCACAGTTGAAGAGCAGGCAGAAGGAGTTGTGA
AGACAGGACAATCTTCTTGGGATGCTGGTCTGGAAAGCCAGCAGGGCCTGCTCTGCTTGGCTCATTGACCC
CAGGTTCTCTGGTTAAACTGAAAGCCTACTACTGGCCTGGTCCCCATCAATCCATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATATGCACTGAGCTCCCTGTTGGCTCTGCTGCGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTCTGGGTCAGCCTGAGCCTCTGCGGGTTCTGGATCCAGGGGAGGGAGAAAG
ATCCCTGTGTCGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAATCCAGATTGAGAGCTCGGCTAGACCAAAGTG
ATGAAGACTTCAAACCCCGATTGTCCTACTACAGGGACCCACAAGCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCCGTGAGCGGTTGCTGGTGGCTGACCTCCGAGCTACACTGTCCA
CTTTGGCCGTGGCTGTGAACCGTACGGTGGCCCATCACTTCCCTCGGTTACTCTACTTCAGTGGCAGCAGGGGG
CCCGGGCTCCAGCAGGGATGCAAGGGTGGTGTCTCATGGGATGAGCGGCCGCTGGCTCATGTCAGAGACCCCTGC
GCCACCTTCACACACACTTGGGGCGACTACGACTGGTTCTCATCATGCAAGGATGACACATATGTGCAAGGCC
CCCGCTGGCAGCCCTGCTGGCCACCTCAGCATCAACCAAGACCTGACTTAGGCCGGCAGAGGAGTTCATGG
GCGCAGGCAGGAGGCCGGTACTGTCTGGGCTTGGCTACCTGTTGTACCGAGTCTCCCTGCTTCATG
GGCCACATCTGGATGGCTGCCAGGGAGACATTCTCAGTGGCCGCTCGACGAGTGGCTGGACGCTGCCCTCATGG
ACTCTCTGGCGTCGGCTGTGTCACAGCACCAAGGGCAGCAGTATGCTCATTTGAACACTGGCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCCGTGCACCCCTGCTCCGAAGGTACCCCTCATGG
ACCGGCTCCACAAACGCTTCAGCGCTCTGGAGTTGGAGCGGCTTACAGTGAATAGAACAACTGAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACCAACTCTCGCTTGAGGTGCTGGCTGGACTACTTCACAGAGCAGCACACCTCTCCTGTCAGATGGGG
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGAGCTGGGTGATGCGTTGGAGACTGCCCTGGAGCAGCTCA
ATCGCGCTATCAGCCCCGCTGCGCTTCCAGAACGAGCGACTGCTCAACGGCTATCGGCCTCCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGGAAATGTGTGACACAGCGTGGGACCGGGGGCCCTGGCTCGCA
GGGTCAAGCCTGCTGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCACTGAGGCCACCGAGTGC
AGCTGGTGTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGCGTTGAGCCAATGTCC
TGGAGCCACGAGAACATGCATTGCTCACCTGTTGCTGGTCTACGGGCCACGAGAACGGTGGCCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAGCAGCGGAGTTAGAGCGACGGTACCCCTGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCCAGGTGCGACTCATGGACGTGGTCTGAAGAACGACCCCTGTGGACACTCTCT
TCTTCCCTTACCAACCGTGTGGACAAGGCCCTGGGCCGAAGTCTCAACCGCTGCGCATGAATGCCATCTG
GGCAGGCCCTTCCAGTCATTCCAGGAGTTCAATCCTGCCCTGTACCCACAGAGATCACCCCCAGGGCCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGTGTGACCCCTCCCGGGGGCTCCTATAGGGGGGAGATTG
ACCGGCAGGCTCTGCGGAGGGCTGCTTACAAACGCTGACTACCTGGCGGCCGAGCCCGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGGCCCTGGAGGGGCTGGAGGTGATGGATGTTCTCCGGTTCTCAGGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACGTTCTCCCTGCGAGACTGCAGCCCCAGGCTCAGTGAAC
AACTCTACCAACCGCTGCCCTCAGCAACCTGGAGGGCTAGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGGCCATAGCACTAGCCGCTGGGGCCCTAACCTCATTACCTTCTTGTCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTAA
ACATGTCTCTGCC

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPDSRARLD
QSDEDFKPRIVPYYRDPNPKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLLLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAOIRNLTVLTPGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTL DLL ECVTQRGHRRALARRVSLLRPLSRVEILPMPYVTEATRVQLVPL
VAEAAAAPAFLEAFAAANVLEPREHALLTLVVYGPREGGRGAPDPFLGVKAAAELERRYPG
TRLAWLAVRAEAPSQVRLMDVVSKKHPVDTLFFLTTWTRPGPEVLRCRMNAISGWQAFFP
VHFQEFNPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCACCGTGGAGAGGAAACCGTGCACCGCTGCCTTCTGTCCCCAAGCC
GTTCTAGACCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTGATGCTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCGATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTGGACAAACACTGTGACAAAGCAG
AGTTCTCAGTTCTGAAAATGTTAAAGTGTGAGTCAATTATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACAAC
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTTCT
CAATATCCCAGAAAAGTGTCTGAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTAATACCAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTAGATGATGGGTATACCGCCTAGGGCATTGGCATATTTCAAT
ATCAGATGCATGTGATGTGATGGGTATACCGCCTAGGGCATTGGCATATTTCAAT
GATGCATTGGTTTCTTACCTCCAAATGGTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTTGTCATTATTGTAGTAGTAACATACATATCAA
TACAGCTGTATGTTCTTTCTTTCTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTTTCTTAAAACACATGAACATTGAAATG
TGTTGAAAGAAGTGTAAAGAATAATAATTGCAAATAACTATTAAATAATTATAT
GTGATAAATTCTAAATTATGAACATTAGAAATCTGTGGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTCTAACATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAACATTAGCTGTGTTCCCTTACTTCTAACACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTCTCAAATGTACAACTAACAGCAACTAAAGAAA
ATTAAAGTGAAGTGTAAAAAT

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLLAAVKETWTKHCDKAEFFSSENVKFESINMDTNMDWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHТИKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCYNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPPNNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCGCTGCCGCTGGCCCTCAGCAACCCCTGACATGGCGCTGAGGCGGCCACCGCGAC
TCCGGCTCTGCCGCTCGGCCCTGACTTCTTCCCTGCTGCTGCTTTCAGGGGCTGCCCTGATAGGGGCTGTAATC
TCAAATCCAGCAATCGAACCCCAAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTTGATCATTACGGATTGCG
AGACAAGTGACCCCCAGGATCGAGTGGAAAGAAAATTCAAGATGAACAAACCACATATGTGTTTTGACAACAAAA
TTCAGGGAGACTTGGCGGGCTGAGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGCTGTAGAGTGCCAAGGCTGTACCAAGTAGGCAAGATGGCAACACTGC
ACTGCCAGGAGAGTGAGGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGATGTACCAACTGCCACGGATT
CCAGAGCCAATCCCAGATTGCAATTCTTCCACTTAAACTCTGAAACAGGCACTTGGTGTCACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCAATTGCTTCAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAAACATGGCGGAATTATTGGGGGGTTCTGGTGTCTTGCTGTACTGGCCCTGA
TCACGTTGGGCATCTGCTGTGCATACAGACGTGGTACTTCATCAACAATAAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACAGATGGAGTTAACTACATCCGCACTGACGAGGGAGGGCACTTCAGACACAAGTCATGTTTG
TGATCTGAGACCCCGGGTGTGGCTGAGAGCGCACAGAGCGCACGTGCACATACCTCTGCTAGAAACTCCTGTC
GGCAGCGAGAGCTGATGCACTCGGACAGAGCTAGACACTCATTCAGAAGCTTCTGTTGGCCAAGTTGACCA
CTACTCTTCTACTCTAACAAAGCCACATGAATAGAAATTTCCTCAAGATGGACCCGGTAAATATAACCAA
GGAAGCGAAACTGGGTGCGTTCACTGAGTTGGTTCTTAATCTGTTCTGGCCTGATTCGGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTAACAGCCGTCTGGCCCTGTGAAGCAGCATGTTCAACCCTGGTC
CAGCAGCCACGACAGCACCATGTGAGATGGCAGGTGGCTGGACAGCACAGCAGCGCATCCGGGGAACCCA
GAAAAGGCTTCTTACACAGCAGCCTACTTCATCGGCCACAGACACACCACCGCAGTTCTTAAAGGCTCTGC
TGATCGGTGTTGCACTGTCATTGGAGAAGCTTTGGATCAGCATTGTAAGGAAACCTCAGGATTTAAGGAAA
GTAAATTGGTTGCTGGAAGAGGGATCTGCTGAGGAACCCCTGCTGTCCAACAGGGTGTCAAGGATTTAAGGAAA
ACCTCGTCTTAGGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTGTTATTTATAAAATT
TACATCTAAATTGGTCAAGGATGTATTGATTATTGAAAAGAAAATTCTATTTAAACTGTAATATATTGT
CATACAATGTTAAATAACCTATTTTAAAGGTTCAACTTAAGGTAGAAGTTCAAGCTACTAGTGTAAAT
TGGAAAATATCAATAATTAGAGTATTTACCCAAGGAATCCTCTATGGAAGTTACTGTGATGTTCTTTCT
CACACAAGTTTACGCCCTTCAACAGGAACCTACACTGTCTACACATCAGACCATAGTTGCTTAGGAAACCTT
TAAAATTCCAGTTAACATGTTGAAATCAGTTGCATCTCTTCAAAAGAACCTCTCAGGTTAGCTTTGA
GCCTCTCTGAGATGACTAGGACAGTCTGTACCCAGAGGCCACCCAGAACGCCCTCAGATGTACATACAGATG
CCAGTCAGCTCTGGGTGCGCCAGGCCCGCCCTGCTAGCTCACTGTCCTGCTGTGCCAGGAGGCC
GCCATCTCTGGCCCTGGCAGTGGCTGCTCCAGTGAGCTTACTCACGTGCCCTTGCTCATCCAGCACAGC
TCTCAGGTGGGACTGCAAGGACACTGGTGTCTCCATGTAGCGTCCCAGCTTGGCTCTGTAACAGACCTCT
TTTTGGTTATGGCTCACAAATAGGGCCCCCAATGCTATTTTTTTTAAAGTTGTTAATTATTGTT
AAGATTGCTAAGGCCAAAGGCAATTGCGAAATCAAGTCTGCAAGTACAATAACATTAAAAGAAAATTGGAT
CCCACGTGTTCTCTTGCACAGAAGAACCCAGACGCCACAGGCTCTGCGCATTTCAAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGCCTTTAAAGAACGTCAAGGTGGAGCAGCCAGGTGAAAGGCTGGCGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAATTGACTTTCAATTTCATCCGCCGAGACACTGCTCCATT
TGTGGGGGACATTGCAACATCACTCAGAACGCTGTGTTCTCAAGAGCAGGTGTTCTCAGCCTCACATGCC
GCCGTGCTGGACTCAGGACTGAAGTGTGAAAGCAAGGAGCTGCTGAGAAGGAGCACTCCACTGTGTGCC
GAATGGCTCTCAACTCACCCTGCTTCACTGCTTCACTGCTTCAAGTGTCTGGGTTTTTAACTTGCAGCTTT
AATTGCAACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTGCAGGCCAGGGCCTGGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGTGCTCCCTGGTGTGCTGCATGGCATCCTGGATGCTAGCATGCAAGTTC
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCTCCCCACCCCTCAGCGTTGGGATTACGCTCCAGCCT
TCTTGGTTGTCAGTGATAGGGTAGCCTTATTGCCCTCTTCACTGCTAACCTTAAACCTTCAACTAGTG
TGGGAACCAGGCTGAAAAGTAGAGAGAAGTGAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTGTTGATTTAAGATATGAATGTGACTCAAGACTCGAGGCCGATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCCA

FIGURE 124

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLSKIWNVRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267